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OM protein - protein search, using sw model

Run on: March 4, 2004, 15:21:50 ; Search time 1.61702 Seconds
                                            (without alignments)
                                            1397.867 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_29Jan04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	100.0	8	2	AAW32551	Aaw32551 Amyloidog
2	40	100.0	8	4	AAE10663	Aae10663 Human amy
3	40	100.0	8	4	AAE02615	Aae02615 Human amy
4	40	100.0	8	5	ABB78624	Abb78624 Human alp
5	40	100.0	8	6	ABU09765	Abu09765 Amyloidog
6	40	100.0	8	6	ABR61959	Abr61959 Human amy
7	40	100.0	8	7	ABW00134	Abw00134 Beta-amyl
8	40	100.0	9	6	ABU79063	Abu79063 Aggregati
9	40	100.0	9	7	ABW00197	Abw00197 Peptide #

10	40	100.0	10	3	AAY79938	Aay79938	Beta-amyl
11	40	100.0	10	4	AAB46226	Aab46226	Human APP
12	40	100.0	10	4	AAB46228	Aab46228	Human APP
13	40	100.0	10	4	AAB46227	Aab46227	Human APP
14	40	100.0	11	2	AAW32560	Aaw32560	Anti-amyl
15	40	100.0	11	4	AAM52586	Aam52586	Peptide #
16	40	100.0	11	5	AAU99431	Aau99431	Human amy
17	40	100.0	11	5	AAE29504	Aae29504	Amyloid b
18	40	100.0	11	6	ABU79013	Abu79013	Amyloidog
19	40	100.0	11	7	ABW00147	Abw00147	Amyloid-b
20	40	100.0	12	6	AAE35466	Aae35466	Abeta pep
21	40	100.0	13	6	AAE35465	Aae35465	Abeta pep
22	40	100.0	13	6	AAE35467	Aae35467	Abeta pep
23	40	100.0	13	6	ADA37467	Ada37467	Human amy
24	40	100.0	14	6	ADA89887	Ada89887	Beta-A4 s
25	40	100.0	15	2	AAW02334	Aaw02334	Beta-amyl
26	40	100.0	15	2	AAW89358	Aaw89358	Beta-amyl
27	40	100.0	15	2	AAW89354	Aaw89354	Beta-amyl
28	40	100.0	15	5	ABG71014	Abg71014	Long form
29	40	100.0	15	5	ABB05162	Abb05162	Beta amyl
30	40	100.0	15	5	AAE26271	Aae26271	Human bet
31	40	100.0	15	6	ABU79057	Abu79057	Aggregati
32	40	100.0	15	6	ABU79064	Abu79064	Aggregati
33	40	100.0	15	6	ABU79055	Abu79055	Aggregati
34	40	100.0	15	6	ABU79056	Abu79056	Aggregati
35	40	100.0	15	6	ABU79062	Abu79062	Aggregati
36	40	100.0	15	7	ABW00190	Abw00190	Peptide #
37	40	100.0	15	7	ABW00198	Abw00198	Peptide #
38	40	100.0	15	7	ABW00189	Abw00189	Peptide #
39	40	100.0	15	7	ABW00191	Abw00191	Peptide #
40	40	100.0	15	7	ABW00196	Abw00196	Peptide #
41	40	100.0	16	5	AAE26330	Aae26330	Human bet
42	40	100.0	17	2	AAR54703	Aar54703	Beta-amyl
43	40	100.0	17	2	AAW18880	Aaw18880	Beta-amyl
44	40	100.0	17	4	AAB91774	Aab91774	Amyloid b
45	40	100.0	17	4	AAB91807	Aab91807	Amyloid b

ALIGNMENTS

RESULT 1
AAW32551
ID   AAW32551 standard; peptide; 8 AA.
XX
AC   AAW32551;
XX
DT   21-JAN-1998 (first entry)
XX
DE   Amyloidogenic sequence amyloid beta-peptide.
XX
KW   Anti-amyloid peptide; iAbeta; abnormal protein folding inhibitor;
KW   Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
KW   human prion disease; Kuru; Creutzfeldt-Jakob disease;
KW   Gerstmann-Straussler-Scheinker Syndrome; animal prion disease;
KW   prion associated human neurodegenerative disease; scrapie;
KW   spongiform encephalopathy; transmissible mink encephalopathy;

CC   A method has been developed for the prevention or treatment of a disorder
CC   or disease associated with the formation of amyloid or amyloid-like
CC   deposits, involving the abnormal folding of a protein or peptide. The
CC   method involves administering an inhibitory peptide which prevents the
CC   abnormal folding or which dissolves existing amyloid or amyloid-like
CC   deposits, where the peptide comprises a sequence of 3-15 amino acid
CC   residues and has a hydrophobic cluster of at least 3 amino acids, where
CC   at least one of the 3 amino acids is a beta-sheet blocking amino acid
CC   residue selected from Pro, Gly, Asn and His. The present sequence
CC   represents an amyloidogenic sequence, amyloid beta- peptide, which is
CC   involved in the formation of several amyloid deposits. The inhibitory
CC   peptide is capable of associating with a structural determinant on the
CC   protein or peptide to structurally block and inhibit the abnormal folding
CC   into amyloid or amyloid-like deposits. The method can be used for
CC   preventing, treating or detecting e.g. Alzheimer's dementia or disease,
CC   Down's syndrome, other amyloidosis disorders, human prion diseases such
CC   as Kuru, Creutzfeldt-Jakob disease, Gerstmann- Straussler-Scheinker
CC   Syndrome, prion associated human neurodegenerative diseases or animal
CC   prion diseases such as scrapie, spongiform encephalopathy, transmissible
CC   mink encephalopathy and chronic wasting disease of mule deer and elk
XX
SQ   Sequence 8 AA;

    Query Match   100.0%;   Score 40;   DB 2;   Length 8;
    Best Local Similarity   100.0%;   Pred. No. 1.4e+06;
    Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
            ||||||||
Db   1 KLVFFAED 8

RESULT 2
AAE10663
ID   AAE10663 standard; peptide; 8 AA.
XX
AC   AAE10663;
XX
DT   10-DEC-2001   (first entry)
XX
DE   Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX
KW   Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KW   Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   alpha-secretase.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Cleavage-site   4. .5
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-00023315.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ, Gurney M;
XX
DR   WPI; 2001-444208/48.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with amyloid
PT   precursor protein processing activity and alpha-secretase activity, for
PT   identifying modulators useful in treating Alzheimer's disease.
XX
PS   Claim 10; Page 163; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC   proteins which lack transmembrane domain or amino terminal domain or
CC   cytoplasmic domain and retains alpha-secretase activity and amyloid
CC   protein precursor (APP) processing activity. The proteins of the
CC   invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC   in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC   activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC   are useful for treating Alzheimer's disease (AD) which causes progressive
CC   dementia with consequent formation of amyloid plaques, neurofibrillary
CC   tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC   for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC   with the substrate under acidic conditions and determining the level of

CC   hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC   precursor protein (APP) substrate alpha-secretase peptide which is used
CC   for determining the enzymatic activity of Asp-1 protein lacking
CC   transmembrane domain (TM) and containing a (His)6 tag
XX
SQ   Sequence 8 AA;

      Query Match   100.0%; Score 40; DB 4; Length 8;
      Best Local Similarity   100.0%; Pred. No. 1.4e+06;
      Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
                | | | | | | | |
Db   1 KLVFFAED 8

RESULT 3
AAE02615
ID   AAE02615 standard; peptide; 8 AA.
XX
AC   AAE02615;
XX
DT   10-AUG-2001   (first entry)
XX
DE   Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX
KW   Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW   Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
KW   beta-secretase.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Cleavage-site   4. .5
XX
PN   WO200123533-A2.
XX
PD   05-APR-2001.
XX
PF   22-SEP-2000; 2000WO-US026080.
XX
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA) PHARMACIA & UPJOHN CO.
XX
PI   Gurney M, Bienkowski MJ;
XX
DR   WPI; 2001-290516/30.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease.
XX
PS   Claim 10; Page 98; 189pp; English.
XX

CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human amyloid precursor
CC   protein (APP) substrate alpha-secretase peptide which is used for
CC   determining the enzymatic activity of Asp-1 deltaTM (His)6 protein
XX
SQ   Sequence 8 AA;

     Query Match   100.0%; Score 40; DB 4; Length 8;
     Best Local Similarity   100.0%; Pred. No. 1.4e+06;
     Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
               ||||||||
Db   1 KLVFFAED 8

RESULT 4
ABB78624
ID   ABB78624 standard; peptide; 8 AA.
XX
AC   ABB78624;
XX
DT   16-JUL-2002   (first entry)
XX
DE   Human alpha secretase (Abeta12-28) peptide SEQ ID NO:73.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-00025934.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
PR   22-SEP-2000; 2000GB-00023315.
XX
PA   (PHAA) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ, Gurney M;
XX
DR   WPI; 2002-397167/43.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT   protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS   Example 15; Page 92; 182pp; English.

XX
CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC   proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the non
CC   -coding strand complementary to a defined 1804 nucleotide sequence (see
CC   ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC   proteolytic activity and lacks nucleotides encoding a transmembrane
CC   domain); (3) a purified polynucleotide (III') comprising a sequence that
CC   hybridises under stringent conditions to (III) (the nucleotide sequence
CC   encodes a polypeptide further lacking a pro-peptide domain corresponding
CC   to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC   comprising (III) or (III'); and (5) a host cell (V) transformed or
CC   transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC   substrate (I) may be used as an enzyme substrate in assays to detect
CC   aspartyl protease activity, (II) and therefore diagnose diseases
CC   associated with aberrant hu-Asp1 expression and activity such as
CC   Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC   hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC   sequence represents a human alpha secretase peptide, which is used in an
CC   example from the present invention
XX
SQ   Sequence 8 AA;

      Query Match   100.0%; Score 40; DB 5; Length 8;
      Best Local Similarity   100.0%; Pred. No. 1.4e+06;
      Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
                ||||||||
Db   1 KLVFFAED 8

RESULT 5
ABU09765
ID   ABU09765 standard; peptide; 8 AA.
XX
AC   ABU09765;
XX
DT   17-JUN-2003   (first entry)
XX
DE   Amyloidogenic Amyloid beta-peptide #1.
XX
KW   Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KW   pathological beta-sheet-rich conformation; Down's syndrome;
KW   amyloidosis disorder; human prion disease; kuru; CJD;
KW   Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker syndrome; GSS;
KW   prion associated human neurodegenerative disease; animal prion disease;
KW   scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
KW   chronic wasting disease.
XX
OS   Homo sapiens.
XX

CC   The invention describes an isolated inhibitory peptide (I) which
CC   interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC   residues on a protein or peptide for amyloid or amyloid-like deposit
CC   formation, and inhibits or structurally blocks the abnormal folding of
CC   proteins and peptides into amyloid or amyloid-like deposits and into
CC   pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC   diseases associated with abnormal protein folding into amyloid or amyloid
CC   -like deposits or into pathological beta-sheet-rich precursors of such
CC   deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC   disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC   (CJD), Gerstmann-Straussler-Scheinker syndrome (GSS), prion associated
CC   human neurodegenerative diseases as well as animal prion diseases such as
CC   scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
CC   chronic wasting disease of mule deer and elk. (I) is also useful for
CC   detecting and diagnosing the presence or absence of amyloid or amyloid-
CC   like deposits in vivo and its precursors. This is the amino acid sequence
CC   of peptide associated with the inhibition of amyloid or amyloid like
CC   deposits
XX
SQ   Sequence 8 AA;

    Query Match   100.0%;   Score 40; DB 6; Length 8;
    Best Local Similarity   100.0%;   Pred. No. 1.4e+06;
    Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   1 KLVFFAED 8

RESULT 6
ABR61959
ID   ABR61959 standard; protein; 8 AA.
XX
AC   ABR61959;

```
   Query Match                 100.0%;   Score 40;   DB 6;   Length 8;
   Best Local Similarity       100.0%;   Pred. No. 1.4e+06;
   Matches     8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy           1 KLVFFAED 8
               ||||||||
Db           1 KLVFFAED 8
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RESULT 7

ABW00134
```
ID    ABW00134 standard; peptide; 8 AA.
XX
AC    ABW00134;
XX
DT    15-JAN-2004   (first entry)
XX
DE    Beta-amyloid peptide.
XX
KW    Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
KW    Alzheimer's disease; beta-amyloid.
XX
OS    Unidentified.
XX
PN    US2003087407-A1.
XX
PD    08-MAY-2003.
XX
PF    06-SEP-2002; 2002US-00235483.
XX
PR    07-JUN-1995;    95US-00478326.
PR    10-APR-1996;    96US-00630645.
PR    12-DEC-1996;    96US-00766596.
XX
PA    (UYNY ) UNIV NEW YORK STATE.
XX
PI    Soto-Jara C,  Baumann MH,  Frangione B;
XX
DR    WPI; 2003-616149/58.
XX
PT    New inhibitory peptide, useful for preparing a composition for
PT    diagnosing, preventing or treating disorders associated with amyloid-like
PT    fibril deposits, e.g. Alzheimer's disease, or prion related
PT    encephalopathies.
XX
PS    Example 1; Fig 1A; 52pp; English.
XX
CC    The invention relates to inhibitory peptide comprising a portion of at
CC    least three amino acid residues and a sequence predicted not to adopt a
CC    beta-sheet structure that associates with a hydrophobic beta-sheet
CC    cluster on a protein or peptide involved in the abnormal folding into a
CC    beta-sheet structure, to structurally block the abnormal folding of the
CC    protein or peptide. The inhibitory peptide is useful for preparing a
CC    composition for preventing, treating or detecting disorders or diseases
CC    associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
CC    prion related encephalopathies. The invention is also useful in gene
CC    therapy. The present sequence is beta-amyloid peptide. This peptide is
CC    involved in the formation of several amyloid deposits
XX
SQ    Sequence 8 AA;

  Query Match            100.0%;  Score 40;  DB 7;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy           1 KLVFFAED 8
               ||||||||
```

RESULT 8
ABU79063
ID   ABU79063 standard; peptide; 9 AA.
XX
AC   ABU79063;
XX
DT   17-JUN-2003   (first entry)
XX
DE   Aggregation blocking peptide #15.
XX
KW   Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KW   pathological beta-sheet-rich conformation; Down's syndrome;
KW   amyloidosis disorder; human prion disease; kuru; CJD;
KW   Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker syndrome; GSS;
KW   prion associated human neurodegenerative disease; animal prion disease;
KW   scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
KW   chronic wasting disease.
XX
OS   Unidentified.
XX
PN   US6462171-B1.
XX
PD   08-OCT-2002.
XX
PF   12-DEC-1996;   96US-00766596.
XX
PR   07-JUN-1995;   95US-00478326.
PR   10-APR-1996;   96US-00630645.
XX
PA   (UYNY) UNIV NEW YORK STATE.
XX
PI   Soto-Jara C, Baumann MH, Frangione B;
XX
DR   WPI; 2003-379012/36.
XX
PT   Novel inhibitory peptides which inhibit and structurally block abnormal
PT   folding of protein into amyloid or amyloid-like deposit and into
PT   pathological beta-sheet rich conformation, useful for treating
PT   Alzheimer's disease.
XX
PS   Disclosure; Col 51-52; 51pp; English.
XX
CC   The invention describes an isolated inhibitory peptide (I) which
CC   interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC   residues on a protein or peptide for amyloid or amyloid-like deposit
CC   formation, and inhibits or structurally blocks the abnormal folding of
CC   proteins and peptides into amyloid or amyloid-like deposits and into
CC   pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC   diseases associated with abnormal protein folding into amyloid or amyloid
CC   -like deposits or into pathological beta-sheet-rich precursors of such
CC   deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC   disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC   (CJD), Gerstmann-Straussler-Scheinker syndrome (GSS), prion associated
CC   human neurodegenerative diseases as well as animal prion diseases such as

    Query Match   100.0%;   Score 40;   DB 6;   Length 9;
    Best Local Similarity   100.0%;   Pred. No. 1.4e+06;
    Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 KLVFFAED 8
               | | | | | | | |
Db   2 KLVFFAED 9

RESULT 9
ABW00197

CC   least three amino acid residues and a sequence predicted not to adopt a
CC   beta-sheet structure that associates with a hydrophobic beta-sheet
CC   cluster on a protein or peptide involved in the abnormal folding into a
CC   beta-sheet structure, to structurally block the abnormal folding of the
CC   protein or peptide. The inhibitory peptide is useful for preparing a
CC   composition for preventing, treating or detecting disorders or diseases
CC   associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
CC   prion related encephalopathies. The invention is also useful in gene
CC   therapy. The present sequence is a peptide used in the invention
XX
SQ   Sequence 9 AA;

        Query Match   100.0%; Score 40; DB 7; Length 9;
        Best Local Similarity   100.0%; Pred. No. 1.4e+06;
          Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
                  ||||||||
Db   2 KLVFFAED 9

RESULT 10
AAY79938
ID   AAY79938 standard; peptide; 10 AA.
XX
AC   AAY79938;
XX
DT   11-MAY-2000   (first entry)
XX
DE   Beta-amyloid recognition peptide SEQ ID NO:3.
XX
KW   Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;
KW   Alzheimer's disease; neuroprotective; nootropic.
XX
OS   Homo sapiens.
XX
PN   US6022859-A.
XX
PD   08-FEB-2000.
XX
PF   14-NOV-1997;   97US-00970833.
XX
PR   15-NOV-1996;   96US-0030840P.
XX
PA   (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI   Murphy RM, Kiessling LL;
XX
DR   WPI; 2000-160387/14.
XX
PT   Beta-amyloid inhibitor useful for treating Alzheimer's disease.
XX
PS   Example; Col 7; 15pp; English.
XX
CC   The present invention describes a beta-amyloid inhibitor peptide. Beta-
CC   amyloid inhibitors have neuroprotective and nootropic properties. The
CC   inhibitor peptides are useful for the treatment of Alzheimer's disease.

RESULT 11
AAB46226
ID   AAB46226 standard; peptide; 10 AA.
XX
AC   AAB46226;
XX
DT   04-APR-2001   (first entry)
XX
DE   Human APP derived immunogenic peptide #22.
XX
KW   Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW   Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW   amyloid precursor protein; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200072880-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US014810.
XX
PR   28-MAY-1999;   99US-00322289.
XX
PA   (NEUR-) NEURALAB LTD.
XX
PI   Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR   WPI; 2001-032104/04.
XX
PT   Preventing or treating a disease associated with amyloid deposits,
PT   especially Alzheimer's disease, comprises administering amyloid specific
PT   antibody.
XX
PS   Disclosure; Fig 19; 143pp; English.
XX
CC   This invention describes a novel method of preventing or treating a
CC   disease associated with amyloid deposits of amyloid precursor protein
CC   (APP) Abeta fragments in the brain of a patient, which comprises
CC   administering to the patient: (a) an antibody that binds to Abeta, the
CC   antibody binds to an amyloid deposit and induces a clearing response (Fc
CC   receptor mediated phagocytosis) against it (b) a polypeptide containing
CC   an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC   that induces an immunogenic response against residues 1-3 to 7-11 of
CC   Abeta. The products of the invention have nootropic and neuroprotective
CC   activity. The method is also useful for monitoring a course of treatment
CC   being administered to a patient e.g. active and passive immunization. The
CC   methods are useful for prophylactic and therapeutic treatment of
CC   Alzheimer's disease
XX
SQ   Sequence 10 AA;

      Query Match   100.0%; Score 40; DB 4; Length 10;
      Best Local Similarity   100.0%; Pred. No. 0.04;
       Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
               ||||||||
Db   3 KLVFFAED 10

RESULT 12
AAB46228
ID   AAB46228 standard; peptide; 10 AA.
XX
AC   AAB46228;
XX
DT   04-APR-2001   (first entry)
XX
DE   Human APP derived immunogenic peptide #24.
XX
KW   Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW   Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW   amyloid precursor protein; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200072880-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US014810.
XX
PR   28-MAY-1999;   99US-00322289.
XX
PA   (NEUR-) NEURALAB LTD.
XX
PI   Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR   WPI; 2001-032104/04.
XX
PT   Preventing or treating a disease associated with amyloid deposits,
PT   especially Alzheimer's disease, comprises administering amyloid specific
PT   antibody.
XX
PS   Disclosure; Fig 19; 143pp; English.
XX
CC   This invention describes a novel method of preventing or treating a
CC   disease associated with amyloid deposits of amyloid precursor protein
CC   (APP) Abeta fragments in the brain of a patient, which comprises

CC   administering to the patient: (a) an antibody that binds to Abeta, the
CC   antibody binds to an amyloid deposit and induces a clearing response (Fc
CC   receptor mediated phagocytosis) against it (b) a polypeptide containing
CC   an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC   that induces an immunogenic response against residues 1-3 to 7-11 of
CC   Abeta. The products of the invention have nootropic and neuroprotective
CC   activity. The method is also useful for monitoring a course of treatment
CC   being administered to a patient e.g. active and passive immunization. The
CC   methods are useful for prophylactic and therapeutic treatment of
CC   Alzheimer's disease
XX
SQ   Sequence 10 AA;

   Query Match   100.0%; Score 40; DB 4; Length 10;
   Best Local Similarity   100.0%; Pred. No. 0.04;
   Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
               ||||||||
Db   1 KLVFFAED 8

RESULT 13
AAB46227
ID   AAB46227 standard; peptide; 10 AA.
XX
AC   AAB46227;
XX
DT   04-APR-2001   (first entry)
XX
DE   Human APP derived immunogenic peptide #23.
XX
KW   Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW   Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW   amyloid precursor protein; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200072880-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US014810.
XX
PR   28-MAY-1999;   99US-00322289.
XX
PA   (NEUR-) NEURALAB LTD.
XX
PI   Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR   WPI; 2001-032104/04.
XX
PT   Preventing or treating a disease associated with amyloid deposits,
PT   especially Alzheimer's disease, comprises administering amyloid specific
PT   antibody.
XX
PS   Disclosure; Fig 19; 143pp; English.

XX
CC   This invention describes a novel method of preventing or treating a
CC   disease associated with amyloid deposits of amyloid precursor protein
CC   (APP) Abeta fragments in the brain of a patient, which comprises
CC   administering to the patient: (a) an antibody that binds to Abeta, the
CC   antibody binds to an amyloid deposit and induces a clearing response (Fc
CC   receptor mediated phagocytosis) against it (b) a polypeptide containing
CC   an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC   that induces an immunogenic response against residues 1-3 to 7-11 of
CC   Abeta. The products of the invention have nootropic and neuroprotective
CC   activity. The method is also useful for monitoring a course of treatment
CC   being administered to a patient e.g. active and passive immunization. The
CC   methods are useful for prophylactic and therapeutic treatment of
CC   Alzheimer's disease
XX
SQ   Sequence 10 AA;

     Query Match   100.0%; Score 40; DB 4; Length 10;
     Best Local Similarity   100.0%; Pred. No. 0.04;
     Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   2 KLVFFAED 9

RESULT 14
AAW32560
ID   AAW32560 standard; peptide; 11 AA.
XX
AC   AAW32560;
XX
DT   21-JAN-1998   (first entry)
XX
DE   Anti-amyloid peptide Abeta inhibiting abnormal protein folding.
XX
KW   Anti-amyloid peptide; iAbeta; abnormal protein folding inhibitor;
KW   Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
KW   human prion disease; Kuru; Creutzfeldt-Jakob disease;
KW   Gerstmann-Straussler-Scheinker Syndrome; animal prion disease;
KW   prion associated human neurodegenerative disease; scrapie;
KW   spongiform encephalopathy; transmissible mink encephalopathy;
KW   chronic wasting disease; mule; deer; elk; human.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9639834-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US010220.
XX
PR   07-JUN-1995;   95US-00478326.
PR   10-APR-1996;   96US-00630645.
XX
PA   (UYNY) UNIV NEW YORK STATE.

PT   New inhibitors of fibrillogenesis proteins or peptides - used for
PT   preventing, treating or detecting amyloidosis disorders such as
PT   Alzheimer's disease.
XX
PS   Example 1; Fig 9; 63pp; English.
XX
CC   A method has been developed for the prevention or treatment of a disorder
CC   or disease associated with the formation of amyloid or amyloid-like
CC   deposits, involving the abnormal folding of a protein or peptide. The
CC   method involves administering an inhibitory peptide which prevents the
CC   abnormal folding or which dissolves existing amyloid or amyloid-like
CC   deposits, where the peptide comprises a sequence of 3-15 amino acid
CC   residues and has a hydrophobic cluster of at least 3 amino acids, where
CC   at least one of the 3 amino acids is a beta-sheet blocking amino acid
CC   residue selected from Pro, Gly, Asn and His. The present sequence
CC   represents an anti-amyloid peptide, Abeta, which inhibits abnormal
CC   protein folding. The inhibitory peptide is capable of associating with a
CC   structural determinant on the protein or peptide to structurally block
CC   and inhibit the abnormal folding into amyloid or amyloid-like deposits.
CC   The method can be used for preventing, treating or detecting e.g.
CC   Alzheimer's dementia or disease, Down's syndrome, other amyloidosis
CC   disorders, human prion diseases such as Kuru, Creutzfeldt-Jakob disease,
CC   Gerstmann-Straussler-Scheinker Syndrome, prion associated human
CC   neurodegenerative diseases or animal prion diseases such as scrapie,
CC   spongiform encephalopathy, transmissible mink encephalopathy and chronic
CC   wasting disease of mule deer and elk
XX
SQ   Sequence 11 AA;

      Query Match   100.0%;   Score 40;   DB 2;   Length 11;
      Best Local Similarity   100.0%;   Pred. No. 0.044;
      Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   2 KLVFFAED 9

RESULT 15
AAM52586
ID   AAM52586 standard; peptide; 11 AA.
XX
AC   AAM52586;
XX
DT   07-FEB-2002   (first entry)
XX
DE   Peptide #16 for illustrating method of anticipating protein interaction.
XX
KW   Protein interaction; biochemistry; molecular biology; drug development;
KW   agrochemical; bioengineering.
XX
OS   Unidentified.

CC   The present invention relates to a method for anticipating interaction
CC   between proteins. The method comprises (1) digesting protein A into
CC   oligopeptides; (2) searching a protein sequence database for polypeptides
CC   (polypeptide C) containing these oligopeptide sequences or D their
CC   homologues; (3) performing a local alignment of A and detected C or D;
CC   and (4) using a value calculated from the amino acid or oligonucleotide
CC   frequencies, anticipating that C or D is polypeptide B that interacts
CC   with A. The method is useful for assaying anticipated information about
CC   proteins in biochemical, molecular biology, drug development,
CC   agrochemical and bioengineering areas. The present sequence was used to
CC   illustrate the method
XX
SQ   Sequence 11 AA;

Query Match   100.0%; Score 40; DB 4; Length 11;
Best Local Similarity   100.0%; Pred. No. 0.044;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
             | | | | | | | |
Db   1 KLVFFAED 8

Search completed: March 4, 2004, 15:35:44
Job time : 2.61702 secs

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:31:20 ; Search time 0.519149 Seconds
                                            (without alignments)
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Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                  4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                  5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % | | | | |
Result No.	Score	Query Match	Length	DB	ID	Description
1	40	100.0	8	2	US-08-630-645-1	Sequence 1, Appli
2	40	100.0	8	4	US-08-766-596A-1	Sequence 1, Appli
3	40	100.0	8	5	PCT-US96-10220-1	Sequence 1, Appli
4	40	100.0	9	4	US-08-766-596A-64	Sequence 64, Appl
5	40	100.0	10	3	US-08-970-833-3	Sequence 3, Appli
6	40	100.0	11	2	US-08-630-645-14	Sequence 14, Appl
7	40	100.0	11	4	US-08-766-596A-14	Sequence 14, Appl
8	40	100.0	11	5	PCT-US96-10220-14	Sequence 14, Appl
9	40	100.0	14	4	US-09-594-366-5	Sequence 5, Appli
10	40	100.0	15	2	US-08-612-785B-14	Sequence 14, Appl
11	40	100.0	15	2	US-08-612-785B-37	Sequence 37, Appl

12	40	100.0	15	4	US-08-617-267C-14	Sequence 14, Appl
13	40	100.0	15	4	US-08-766-596A-56	Sequence 56, Appl
14	40	100.0	15	4	US-08-766-596A-57	Sequence 57, Appl
15	40	100.0	15	4	US-08-766-596A-58	Sequence 58, Appl
16	40	100.0	15	4	US-08-766-596A-63	Sequence 63, Appl
17	40	100.0	15	4	US-08-766-596A-65	Sequence 65, Appl
18	40	100.0	17	4	US-09-264-709A-2	Sequence 2, Appli
19	40	100.0	17	4	US-09-594-366-3	Sequence 3, Appli
20	40	100.0	19	3	US-08-970-833-11	Sequence 11, Appl
21	40	100.0	20	3	US-08-970-833-10	Sequence 10, Appl
22	40	100.0	26	1	US-08-304-585-7	Sequence 7, Appli
23	40	100.0	28	1	US-08-346-849-4	Sequence 4, Appli
24	40	100.0	28	1	US-08-302-808-7	Sequence 7, Appli
25	40	100.0	28	2	US-08-609-090-2	Sequence 2, Appli
26	40	100.0	28	2	US-08-986-948-7	Sequence 7, Appli
27	40	100.0	28	2	US-08-293-284A-4	Sequence 4, Appli
28	40	100.0	28	2	US-08-461-216-2	Sequence 2, Appli
29	40	100.0	28	3	US-09-388-890-2	Sequence 2, Appli
30	40	100.0	28	3	US-09-388-890-3	Sequence 3, Appli
31	40	100.0	28	3	US-09-388-890-4	Sequence 4, Appli
32	40	100.0	28	3	US-09-388-890-5	Sequence 5, Appli
33	40	100.0	28	3	US-09-388-890-6	Sequence 6, Appli
34	40	100.0	28	3	US-09-388-890-7	Sequence 7, Appli
35	40	100.0	28	3	US-09-388-890-8	Sequence 8, Appli
36	40	100.0	28	3	US-09-388-890-9	Sequence 9, Appli
37	40	100.0	28	3	US-09-388-890-10	Sequence 10, Appl
38	40	100.0	28	3	US-09-388-890-14	Sequence 14, Appl
39	40	100.0	28	4	US-09-264-709A-1	Sequence 1, Appli
40	40	100.0	28	4	US-08-723-661B-2	Sequence 2, Appli
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44	40	100.0	28	4	US-09-660-954-5	Sequence 5, Appli
45	40	100.0	28	4	US-09-660-954-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-630-645-1
; Sequence 1, Application US/08630645
; Patent No. 5948763
;   GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio
;   APPLICANT: BAUMANN, Marc
;   APPLICANT: FRANGIONE, Blas
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;   TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED
;   TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK
;   STREET: 419 Seventh Street, N.W., Suite 400
;   CITY: Washington

US-08-630-645-1

   Query Match   100.0%; Score 40; DB 2; Length 8;
   Best Local Similarity   100.0%; Pred. No. 3e+05;
   Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy           1 KLVFFAED 8
               ||||||||
Db           1 KLVFFAED 8
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RESULT 2
US-08-766-596A-1
; Sequence 1, Application US/08766596A
; Patent No. 6462171
;   GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio
;   APPLICANT: BAUMANN, Marc
;   APPLICANT: FRANGIONE, Blas
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;   TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;   TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;   TITLE OF INVENTION: DEPOSITS
;   NUMBER OF SEQUENCES: 69
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK

US-08-766-596A-1

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Query Match              100.0%;  Score 40;  DB 4;  Length 8;
Best Local Similarity    100.0%;  Pred. No. 3e+05;
Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8
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RESULT 3
PCT-US96-10220-1
; Sequence 1, Application PC/TUS9610220
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;   TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED
;   TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:

; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
PCT-US96-10220-1

   Query Match   100.0%; Score 40; DB 5; Length 8;
   Best Local Similarity   100.0%; Pred. No. 3e+05;
   Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   1 KLVFFAED 8

RESULT 4
US-08-766-596A-64
; Sequence 64, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio
;   APPLICANT: BAUMANN, Marc
;   APPLICANT: FRANGIONE, Blas
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;   TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES

;   TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;   TITLE OF INVENTION: DEPOSITS
;   NUMBER OF SEQUENCES: 69
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK
;   STREET: 419 Seventh Street, N.W., Suite 400
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20004
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/766,596A
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/630,645
;   FILING DATE: 10-APR-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/478,326
;   FILING DATE: 06-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: YUN, Allen C.
;   REGISTRATION NUMBER: 37,971
;   REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 64:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-766-596A-64

  Query Match   100.0%;   Score 40;   DB 4;   Length 9;
  Best Local Similarity   100.0%;   Pred. No. 3e+05;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
             ||||||||
Db   2 KLVFFAED 9

RESULT 5
US-08-970-833-3
; Sequence 3, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
;   APPLICANT: Kiessling, Laura L.

US-08-970-833-3

   Query Match   100.0%; Score 40; DB 3; Length 10;
   Best Local Similarity   100.0%; Pred. No. 0.015;
   Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   1 KLVFFAED 8

RESULT 6
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
;   GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio
;   APPLICANT: BAUMANN, Marc
;   APPLICANT: FRANGIONE, Blas
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;   TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED
;   TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS

```
;     NUMBER OF SEQUENCES:  26
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BROWDY AND NEIMARK
;       STREET:  419 Seventh Street, N.W., Suite 400
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/630,645
;       FILING DATE:
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/478,326
;       FILING DATE:  06-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  YUN, Allen C.
;       REGISTRATION NUMBER:  37,971
;       REFERENCE/DOCKET NUMBER:  SOTO-JARA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-630-645-14

   Query Match                100.0%;  Score 40;  DB 2;  Length 11;
   Best Local Similarity   100.0%;  Pred. No. 0.017;
   Matches     8; Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9


RESULT 7
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
;  GENERAL INFORMATION:
;     APPLICANT:  SOTO-JARA, Claudio
;     APPLICANT:  BAUMANN, Marc
;     APPLICANT:  FRANGIONE, Blas
;     TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL
;     TITLE OF INVENTION:  COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
```

;   TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;   TITLE OF INVENTION: DEPOSITS
;   NUMBER OF SEQUENCES: 69
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK
;   STREET: 419 Seventh Street, N.W., Suite 400
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20004
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/766,596A
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/630,645
;   FILING DATE: 10-APR-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/478,326
;   FILING DATE: 06-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: YUN, Allen C.
;   REGISTRATION NUMBER: 37,971
;   REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-766-596A-14

  Query Match   100.0%; Score 40; DB 4; Length 11;
  Best Local Similarity   100.0%; Pred. No. 0.017;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
           | | | | | | | |
Db   2 KLVFFAED 9

RESULT 8
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

;   TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED
;   TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK
;   STREET: 419 Seventh Street, N.W., Suite 400
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20004
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US96/10220
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/478,326
;   FILING DATE: 06-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/630,645
;   FILING DATE: 10-APR-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: BROWDY, Roger L.
;   REGISTRATION NUMBER: 25,618
;   REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
PCT-US96-10220-14

   Query Match   100.0%; Score 40; DB 5; Length 11;
   Best Local Similarity   100.0%; Pred. No. 0.017;
   Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
             ||||||||
Db   2 KLVFFAED 9

RESULT 9
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor

```
  Query Match                100.0%;  Score 40;  DB 4;  Length 14;
  Best Local Similarity      100.0%;  Pred. No. 0.021;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 KLVFFAED 8
              ||||||||
Db          4 KLVFFAED 11
```

RESULT 10
US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
;   GENERAL INFORMATION:
;   APPLICANT: Findeis, Mark A. et al.
;   TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
;   TITLE OF INVENTION: Aggregation
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 28 State Street, Suite 510
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/612,785B
;   FILING DATE: Herewith
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/404,831
;   FILING DATE: 14-MAR-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/475,579
;   FILING DATE: 07-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/548,998
;   FILING DATE: 27-OCT-1995

; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
US-08-612-785B-14

   Query Match   100.0%; Score 40; DB 2; Length 15;
   Best Local Similarity   100.0%; Pred. No. 0.023;
   Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   1 KLVFFAED 8

RESULT 11
US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
;   APPLICANT: Findeis, Mark A. et al.
;   TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
;   TITLE OF INVENTION: Aggregation
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 28 State Street, Suite 510
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/612,785B
;   FILING DATE: Herewith
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/404,831
;   FILING DATE: 14-MAR-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/475,579
;   FILING DATE: 07-JUN-1995
;   PRIOR APPLICATION DATA:

; INFORMATION FOR SEQ ID NO: 37:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
US-08-612-785B-37

   Query Match   100.0%; Score 40; DB 2; Length 15;
   Best Local Similarity   100.0%; Pred. No. 0.023;
   Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
             ||||||||
Db   6 KLVFFAED 13

RESULT 12
US-08-617-267C-14
; Sequence 14, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
;   APPLICANT: Findeis, Mark A. et al.
;   TITLE OF INVENTION: Modulators of Amyloid Aggregation
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD, LLP
;   STREET: 28 State Street
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/617,267C
;   FILING DATE: 14-MAR-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/404,831
;   FILING DATE: 14-MAR-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/475,579
;   FILING DATE: 07-JUN-1995
;   PRIOR APPLICATION DATA:

; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
US-08-617-267C-14

   Query Match   100.0%; Score 40; DB 4; Length 15;
   Best Local Similarity 100.0%; Pred. No. 0.023;
   Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
             ||||||||
Db   1 KLVFFAED 8

RESULT 13
US-08-766-596A-56
; Sequence 56, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio
;   APPLICANT: BAUMANN, Marc
;   APPLICANT: FRANGIONE, Blas
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;   TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;   TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;   TITLE OF INVENTION: DEPOSITS
;   NUMBER OF SEQUENCES: 69
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK
;   STREET: 419 Seventh Street, N.W., Suite 400
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20004
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/766,596A
;   FILING DATE:

```
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,645
;      FILING DATE:  10-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/478,326
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YUN, Allen C.
;      REGISTRATION NUMBER:  37,971
;      REFERENCE/DOCKET NUMBER:  SOTO-JARA=1A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-766-596A-56

   Query Match              100.0%;  Score 40;  DB 4;  Length 15;
   Best Local Similarity    100.0%;  Pred. No. 0.023;
   Matches    8;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy           1 KLVFFAED 8
               ||||||||
Db           5 KLVFFAED 12



RESULT 14
US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
;  GENERAL INFORMATION:
;    APPLICANT:  SOTO-JARA, Claudio
;    APPLICANT:  BAUMANN, Marc
;    APPLICANT:  FRANGIONE, Blas
;    TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL
;    TITLE OF INVENTION:  COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;    TITLE OF INVENTION:  ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;    TITLE OF INVENTION:  DEPOSITS
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 400
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/766,596A
;       FILING DATE:
;       CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/630,645
;       FILING DATE:  10-APR-1996
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/478,326
;       FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  YUN, Allen C.
;       REGISTRATION NUMBER:  37,971
;       REFERENCE/DOCKET NUMBER:  SOTO-JARA=1A
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-766-596A-57

  Query Match              100.0%;  Score 40;  DB 4;  Length 15;
  Best Local Similarity    100.0%;  Pred. No. 0.023;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              | | | | | | | |
Db          5 KLVFFAED 12


RESULT 15
US-08-766-596A-58
; Sequence 58, Application US/08766596A
; Patent No. 6462171
;  GENERAL INFORMATION:
;    APPLICANT:  SOTO-JARA, Claudio
;    APPLICANT:  BAUMANN, Marc
;    APPLICANT:  FRANGIONE, Blas
;    TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL
;    TITLE OF INVENTION:  COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;    TITLE OF INVENTION:  ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;    TITLE OF INVENTION:  DEPOSITS
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BROWDY AND NEIMARK
;       STREET:  419 Seventh Street, N.W., Suite 400
;       CITY:  Washington
;       STATE:  D.C.
```

```
;         COUNTRY:  USA
;         ZIP:  20004
;      COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  PC-DOS/MS-DOS
;        SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/08/766,596A
;        FILING DATE:
;        CLASSIFICATION:  435
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 08/630,645
;        FILING DATE:  10-APR-1996
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 08/478,326
;        FILING DATE:  06-JUN-1995
;      ATTORNEY/AGENT INFORMATION:
;        NAME:  YUN, Allen C.
;        REGISTRATION NUMBER:  37,971
;        REFERENCE/DOCKET NUMBER:  SOTO-JARA=1A
;      TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  202-628-5197
;        TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  58:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH:  15 amino acids
;        TYPE:  amino acid
;        STRANDEDNESS:  single
;        TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
US-08-766-596A-58

   Query Match              100.0%;  Score 40;  DB 4;  Length 15;
   Best Local Similarity    100.0%;  Pred. No. 0.023;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 KLVFFAED 8
               ||||||||
Db           5 KLVFFAED 12


Search completed: March  4, 2004, 15:42:14
Job time : 0.519149 secs
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OM protein - protein search, using sw model

Run on: March 4, 2004, 15:30:05 ; Search time 0.434043 Seconds
                                             (without alignments)
                                             1772.942 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_78:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

          %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   40 100.0   33   2   S23094   beta-amyloid prote
     2   40 100.0   42   2   PN0512   beta-amyloid prote
     3   40 100.0   57   2   E60045   Alzheimer's diseas
     4   40 100.0   57   2   F60045   Alzheimer's diseas
     5   40 100.0   57   2   G60045   Alzheimer's diseas
     6   40 100.0   57   2   D60045   Alzheimer's diseas
     7   40 100.0   57   2   A60045   Alzheimer's diseas
     8   40 100.0   57   2   B60045   Alzheimer's diseas
     9   40 100.0   82   2   PQ0438   Alzheimer's diseas
    10   40 100.0   695   1   A49795   Alzheimer's diseas
    11   40 100.0   695   2   A27485   Alzheimer's diseas
    12   40 100.0   695   2   S00550   Alzheimer's diseas
    13   40 100.0   770   1   QRHUA4   Alzheimer's diseas

```
14      36    90.0     747    2    JH0773          Alzheimer's diseas
15      34    85.0     321    2    H71729          hypothetical prote
16      32    80.0     182    2    T35807          hypothetical prote
17      32    80.0     261    2    B89868          conserved hypothet
18      31    77.5     119    2    D69345          LSU ribosomal prot
19      31    77.5     641    2    H69651          lichenan operon tr
20      31    77.5    1339    2    T38991          conserved hypothet
21      31    77.5    1364    2    T51920          probable xanthine
22      30    75.0     222    2    T24151          hypothetical prote
23      30    75.0     258    2    AG0459          Sec-independent pr
24      30    75.0     341    2    A64383          hypothetical prote
25      30    75.0     370    2    T47131          G-protein coupled
26      30    75.0     502    2    T27908          hypothetical prote
27      30    75.0     533    2    T46975          lysine-tRNA ligase
28      30    75.0     681    2    T39814          hypothetical prote
29      30    75.0     740    2    S61568          probable membrane
30      30    75.0     768    2    T45876          hypothetical prote
31      30    75.0    1353    2    JC4279          adenylate cyclase
32      29    72.5      99    2    F95064          ribosomal protein
33      29    72.5      99    2    H97931          conserved hypothet
34      29    72.5     100    2    AH1192          B. subtilis YneR p
35      29    72.5     116    1    R5HSS6          ribosomal protein
36      29    72.5     152    2    T06645          hypothetical prote
37      29    72.5     162    2    T13487          NADH2 dehydrogenas
38      29    72.5     162    2    T13563          NADH2 dehydrogenas
39      29    72.5     162    2    T13656          NADH2 dehydrogenas
40      29    72.5     162    2    T13659          NADH2 dehydrogenas
41      29    72.5     164    2    T13562          NADH2 dehydrogenas
42      29    72.5     189    2    S39864          late competence op
43      29    72.5     231    2    H85138          hypothetical prote
44      29    72.5     247    2    B86301          hypothetical prote
45      29    72.5     258    1    S39747          ywfN protein - Bac
```

ALIGNMENTS

RESULT 1
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic
proteinase.
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology

    Query Match   100.0%; Score 40; DB 2; Length 33;
    Best Local Similarity   100.0%; Pred. No. 0.045;
    Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 2
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.;
Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid
protein fragment for NK-1 substance p receptors.
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid

   Query Match             100.0%;  Score 40;  DB 2;  Length 42;
   Best Local Similarity   100.0%;  Pred. No. 0.057;
   Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         16 KLVFFAED 23


RESULT 3
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

   Query Match             100.0%;  Score 40;  DB 2;  Length 57;
   Best Local Similarity   100.0%;  Pred. No. 0.078;
   Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 4
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

   Query Match            100.0%;  Score 40;  DB 2;  Length 57;
   Best Local Similarity  100.0%;  Pred. No. 0.078;
   Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 5
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

   Query Match            100.0%;  Score 40;  DB 2;  Length 57;
   Best Local Similarity  100.0%;  Pred. No. 0.078;
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     Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 6
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

   Query Match              100.0%;  Score 40;  DB 2;  Length 57;
   Best Local Similarity    100.0%;  Pred. No. 0.078;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 7
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

   Query Match              100.0%;  Score 40;  DB 2;  Length 57;
```

```
   Best Local Similarity   100.0%;  Pred. No. 0.078;
   Matches   8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 KLVFFAED 8
            | | | | | | | |
Db       21 KLVFFAED 28



RESULT 8
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: B60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: B60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

   Query Match              100.0%;  Score 40;  DB 2;  Length 57;
   Best Local Similarity    100.0%;  Pred. No. 0.078;
   Matches   8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 KLVFFAED 8
            | | | | | | | |
Db       21 KLVFFAED 28



RESULT 9
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid
precursor protein gene.
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
```

A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

```
   Query Match              100.0%;  Score 40;  DB 2;  Length 82;
   Best Local Similarity    100.0%;  Pred. No. 0.11;
   Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 KLVFFAED 8
               ||||||||
Db          32 KLVFFAED 39
```


RESULT 10
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human
supports a primate model for beta amyloidosis in Alzheimer's disease.
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing

```
   Query Match              100.0%;  Score 40;  DB 1;  Length 695;
   Best Local Similarity    100.0%;  Pred. No. 1;
   Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 KLVFFAED 8
               ||||||||
Db         612 KLVFFAED 619
```


RESULT 11
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; transmembrane protein

```
   Query Match               100.0%;  Score 40;  DB 2;  Length 695;
   Best Local Similarity   100.0%;  Pred. No. 1;
   Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 KLVFFAED 8
              ||||||||
Db        612 KLVFFAED 619
```

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550

A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate
proteoglycan core protein.
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of
rat brain.
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or
plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

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    Query Match              100.0%;  Score 40;  DB 2;  Length 695;
    Best Local Similarity    100.0%;  Pred. No. 1;
    Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              | | | | | | | |
Db        612 KLVFFAED 619
```

RESULT 13
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor
XIa inhibitor; proteinase nexin II (PN-II)
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short,
vascular form; amyloid protein precursor splice form APP(695); amyloid protein
precursor splice form APP(751); amyloid protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453;
I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925;
A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038;

S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186;
S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck,
A.; Beyreuther, K.; Mueller-Hill, B.
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is
encoded by 16 exons.
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the
beta-protein precursor gene.
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1;
PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little,
S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows
similarity to soybean trypsin inhibitor.
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.;
Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in
amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein
diagnostic assays.
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452

A;Status: nucleic acid sequence not shown; translation not shown; translated
from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated
from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.;
van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral
hemorrhage, Dutch type.
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary
Alzheimer's disease.
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.;
Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.;
Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma,
V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.;
Schellenberg, G.D.
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds
for the APP gene region.
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380

A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.;
Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a
cell-surface receptor.
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the
cerebrovascular and the neuritic plaque amyloid peptides.
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain
amyloid of Alzheimer's disease.
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop,
P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage
near the Alzheimer locus.
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang,
J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid
A4 precursor of Alzheimer's disease.
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella,
J.F.; Neve, R.L.
Nature 331, 528-530, 1988

A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA
associated with Alzheimer's disease.
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.;
Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase
inhibitors.
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1;
PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease
inhibitory activity.
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer,
B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of
three patients with sporadic Alzheimer's disease.
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.;
Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
disease brain: coding and noncoding regions of the fetal precursor mRNA are
expressed in the cortex.
A;Reference number: A31087; MUID:88124954; PMID:2893379

A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for
residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT
for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn,
AAT for residue 610 as Gly, and GGT for residue 655 as Ser
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.;
Beyreuther, K.

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Qy   1 KLVFFAED 8
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Db   687 KLVFFAED 694

RESULT 14
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein:
developmental regulation of its gene expression.
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

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Qy   1 KLVFFAED 8
              | | | | | | | :
Db   664 KLVFFAEE 671

RESULT 15
H71729
hypothetical protein RP189 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: H71729

R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.;
Alsmark, U.C.M.; Podowski, R.M.; Naeslund, A.K.; Eriksson, A.S.; Winkler, H.H.;
Kurland, C.G.
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71729
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-321 <AND>
A;Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14655.1;
PID:e1342498; PID:g3860754; GSPDB:GN00081
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: RP189
C;Superfamily: Rickettsia prowazekii hypothetical protein RP189

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Qy   1 KLVFFAED 8
              ||:||| |
Db   178 KLIFFAHD 185

Search completed: March 4, 2004, 15:41:01
Job time : 1.43404 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 15:39:01 ; Search time 0.893617 Seconds
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                                           1890.324 Million cell updates/sec

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Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

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                                SUMMARIES
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Result   Query
   No.   Score   Match Length DB   ID   Description

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    2      40   100.0      9    9   US-09-899-815-2         Sequence 2, Appli
    3      40   100.0      9   14   US-10-235-483-64        Sequence 64, Appl
    4      40   100.0     11    9   US-09-988-842-9         Sequence 9, Appli
    5      40   100.0     11    9   US-09-988-842-25        Sequence 25, Appl
    6      40   100.0     11   14   US-10-235-483-14        Sequence 14, Appl
    7      40   100.0     13   14   US-10-281-458-1         Sequence 1, Appli
    8      40   100.0     14    9   US-09-992-800-5         Sequence 5, Appli
    9      40   100.0     14    9   US-09-992-994-5         Sequence 5, Appli
   10      40   100.0     14   15   US-10-385-065-5         Sequence 5, Appli
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   23      40   100.0     19   10   US-09-825-242-5         Sequence 5, Appli
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   26      40   100.0     28    9   US-09-867-847-4         Sequence 4, Appli
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   32      40   100.0     33   10   US-09-930-915A-295      Sequence 295, App
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   35      40   100.0     35    9   US-09-867-847-3         Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-10-235-483-1
; Sequence 1, Application US/10235483
; Publication No. US20030087407A1
;   GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio

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   Best Local Similarity    100.0%;  Pred. No. 7.1e+05;
   Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 KLVFFAED 8
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Db          1 KLVFFAED 8
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RESULT 2
US-09-899-815-2
; Sequence 2, Application US/09899815
; Patent No. US20020162129A1
; GENERAL INFORMATION:
; APPLICANT: LANNFELT, Lars
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: LANNFELT=1A
; CURRENT APPLICATION NUMBER: US/09/899,815
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,098
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: EP 00202387.7
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide (16-24 of SEQ ID NO:1)
US-09-899-815-2

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  Best Local Similarity   100.0%; Pred. No. 7.1e+05;
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Qy   1 KLVFFAED 8
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Db   1 KLVFFAED 8

RESULT 3
US-10-235-483-64
; Sequence 64, Application US/10235483
; Publication No. US20030087407A1
;   GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio
;   BAUMANN, Marc
;   FRANGIONE, Blas
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;   COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;   ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;   DEPOSITS
;   NUMBER OF SEQUENCES: 69
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK
;   STREET: 419 Seventh Street, N.W., Suite 400
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20004
;   COMPUTER READABLE FORM:

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;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: PC-DOS/MS-DOS
;               SOFTWARE: PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/10/235,483
;               FILING DATE: 06-Sep-2002
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: US/08/766,596
;               FILING DATE: <Unknown>
;               APPLICATION NUMBER: US 08/630,645
;               FILING DATE: 10-APR-1996
;               APPLICATION NUMBER: US 08/478,326
;               FILING DATE: 06-JUN-1995
;          ATTORNEY/AGENT INFORMATION:
;               NAME: YUN, Allen C.
;               REGISTRATION NUMBER: 37,971
;               REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: 202-628-5197
;               TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 64:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 9 amino acids
;               TYPE: amino acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-235-483-64

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Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9



RESULT 4
US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
;  APPLICANT: Johansson, Jan
;  TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
;  TITLE OF INVENTION:  OF AMYLOID FORMATION
;  FILE REFERENCE: 12125-002001
;  CURRENT APPLICATION NUMBER: US/09/988,842
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: US 60/251,662
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: US 60/253,695
;  PRIOR FILING DATE: 2000-11-20
;  NUMBER OF SEQ ID NOS: 26
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;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

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Qy   1 KLVFFAED 8
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Db   2 KLVFFAED 9

RESULT 5
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
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;   OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

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Qy   1 KLVFFAED 8
               |||||||||
Db   2 KLVFFAED 9

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; Publication No. US20030087407A1
;   GENERAL INFORMATION:

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Qy          1 KLVFFAED 8
              | | | | | | | |
Db          2 KLVFFAED 9
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RESULT 7
US-10-281-458-1
; Sequence 1, Application US/10281458
; Publication No. US20030108978A1
; GENERAL INFORMATION:
; APPLICANT: Ciambrone, Gary J.
; APPLICANT: Gibbons, Ian
; TITLE OF INVENTION: Whole Cell Assay Systems for Cell
; TITLE OF INVENTION: Surface Proteases
; FILE REFERENCE: 50225-8093.US03
; CURRENT APPLICATION NUMBER: US/10/281,458
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/337,641
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/924,692
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-281-458-1

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Qy   1 KLVFFAED 8
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Db   6 KLVFFAED 13

RESULT 8
US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. US20020102261A1
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
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US-09-992-800-5

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Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


Qy          1 KLVFFAED 8
              ||||||||
Db          4 KLVFFAED 11



RESULT 9
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; Sequence 5, Application US/09992994
; Patent No. US20020136718A1
; GENERAL INFORMATION:
;  APPLICANT: Raso, Victor
;  TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
;  FILE REFERENCE: BBRI-2005
;  CURRENT APPLICATION NUMBER: US/09/992,994
;  CURRENT FILING DATE:  2001-11-06
;  PRIOR APPLICATION NUMBER: 09/594,366
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/139,408
;  PRIOR FILING DATE: 1999-06-16
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;    LENGTH: 14
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-992-994-5

  Query Match              100.0%;  Score 40;  DB 9;  Length 14;
  Best Local Similarity    100.0%;  Pred. No. 0.077;
  Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


Qy          1 KLVFFAED 8
              ||||||||
Db          4 KLVFFAED 11



RESULT 10
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; Publication No. US20030235897A1
; GENERAL INFORMATION:
;  APPLICANT: Raso, Victor
;  TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
;  FILE REFERENCE: BBRI-2004
;  CURRENT APPLICATION NUMBER: US/10/385,065
;  CURRENT FILING DATE:  2003-03-10
;  PRIOR APPLICATION NUMBER: US/09/594,366
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/139,408
;  PRIOR FILING DATE: 1999-06-16
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
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;    LENGTH: 14
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-385-065-5

   Query Match              100.0%;  Score 40;  DB 15;  Length 14;
   Best Local Similarity    100.0%;  Pred. No. 0.077;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy         1 KLVFFAED 8
             ||||||||
Db         4 KLVFFAED 11



RESULT 11
US-09-972-475-14
; Sequence 14, Application US/09972475
; Patent No. US20020098173A1
;    GENERAL INFORMATION:
;         APPLICANT: Findeis, Mark A. et al.
;         TITLE OF INVENTION: Modulators of Amyloid Aggregation
;         NUMBER OF SEQUENCES: 45
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: LAHIVE & COCKFIELD, LLP
;              STREET: 28 State Street
;              CITY: Boston
;              STATE: Massachusetts
;              COUNTRY: USA
;              ZIP: 02109-1875
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/972,475
;              FILING DATE: 04-Oct-2001
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/617,267
;              FILING DATE: <Unknown>
;              APPLICATION NUMBER: USSN 08/475,579
;              FILING DATE: 07-JUN-1995
;              APPLICATION NUMBER: USSN 08/548,998
;              FILING DATE: 27-OCT-1995
;         ATTORNEY/AGENT INFORMATION:
;              NAME: DeConti, Giulio A.
;              REGISTRATION NUMBER: 31,503
;              REFERENCE/DOCKET NUMBER: PPI-002CP2
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (617)227-7400
;              TELEFAX: (617)227-5941
;    INFORMATION FOR SEQ ID NO: 14:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 15 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: peptide
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;          FRAGMENT TYPE: internal
;          SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-972-475-14

   Query Match            100.0%;  Score 40;  DB 9;  Length 15;
   Best Local Similarity  100.0%;  Pred. No. 0.082;
   Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8


RESULT 12
US-09-996-357-9
; Sequence 9, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
;  APPLICANT: Gefter, Malcolm L
;  APPLICANT:  Isreal, David I
;  APPLICANT:  Joyal, John L
;  APPLICANT:  Gosselin, Michael
;  TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
;  TITLE OF INVENTION:  TREATING AN AMYLOIDOGENIC DISEASE
;  FILE REFERENCE: PPI-105
;  CURRENT APPLICATION NUMBER: US/09/996,357
;  CURRENT FILING DATE:  2001-11-27
;  PRIOR APPLICATION NUMBER: 60/253,302
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/250,198
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 60/257,186
;  PRIOR FILING DATE: 2000-12-20
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;    LENGTH: 15
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-996-357-9

   Query Match            100.0%;  Score 40;  DB 9;  Length 15;
   Best Local Similarity  100.0%;  Pred. No. 0.082;
   Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8


RESULT 13
US-10-235-483-56
; Sequence 56, Application US/10235483
; Publication No. US20030087407A1
;   GENERAL INFORMATION:
;        APPLICANT: SOTO-JARA, Claudio
;                   BAUMANN, Marc
```

    Query Match   100.0%;   Score 40;   DB 14;   Length 15;
    Best Local Similarity   100.0%;   Pred. No. 0.082;
    Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
               | | | | | | | |
Db   5 KLVFFAED 12

RESULT 14
US-10-235-483-57
; Sequence 57, Application US/10235483
; Publication No. US20030087407A1
;   GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio
;   BAUMANN, Marc
;   FRANGIONE, Blas
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;   COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;   ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;   DEPOSITS
;   NUMBER OF SEQUENCES: 69
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK
;   STREET: 419 Seventh Street, N.W., Suite 400
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20004
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/235,483
;   FILING DATE: 06-Sep-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/766,596
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: US 08/630,645
;   FILING DATE: 10-APR-1996
;   APPLICATION NUMBER: US 08/478,326
;   FILING DATE: 06-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: YUN, Allen C.
;   REGISTRATION NUMBER: 37,971
;   REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 57:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-235-483-57

   Query Match   100.0%; Score 40; DB 14; Length 15;
   Best Local Similarity   100.0%; Pred. No. 0.082;

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     Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 KLVFFAED 8
             ||||||||
Db         5 KLVFFAED 12


RESULT 15
US-10-235-483-58
; Sequence 58, Application US/10235483
; Publication No. US20030087407A1
;   GENERAL INFORMATION:
;         APPLICANT: SOTO-JARA, Claudio
;                    BAUMANN, Marc
;                    FRANGIONE, Blas
;         TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;                              COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;                              ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;                              DEPOSITS
;         NUMBER OF SEQUENCES: 69
;         CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 400
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/235,483
;             FILING DATE: 06-Sep-2002
;             CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/766,596
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 08/630,645
;             FILING DATE: 10-APR-1996
;             APPLICATION NUMBER: US 08/478,326
;             FILING DATE: 06-JUN-1995
;         ATTORNEY/AGENT INFORMATION:
;             NAME: YUN, Allen C.
;             REGISTRATION NUMBER: 37,971
;             REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;         TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 58:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
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  Query Match   100.0%;   Score 40;   DB 14;   Length 15;
  Best Local Similarity   100.0%;   Pred. No. 0.082;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   5 KLVFFAED 12

Search completed: March 4, 2004, 15:57:37
Job time : 0.893617 secs

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:28:35 ; Search time 1.14894 Seconds
                                             (without alignments)
                                             2196.942 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_25:*
                 1:   sp_archea:*
                 2:   sp_bacteria:*
                 3:   sp_fungi:*
                 4:   sp_human:*
                 5:   sp_invertebrate:*
                 6:   sp_mammal:*
                 7:   sp_mhc:*
                 8:   sp_organelle:*
                 9:   sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*
                 15: sp_rvirus:*
                 16: sp_bacteriap:*
                 17: sp_archeap:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description

1	40	100.0	28	4	Q9UCD1	Q9ucd1 homo sapien
2	40	100.0	30	4	Q9UCA9	Q9uca9 homo sapien
3	40	100.0	33	4	Q9UC33	Q9uc33 homo sapien
4	40	100.0	79	11	O35463	O35463 cricetulus
5	40	100.0	82	4	Q16020	Q16020 homo sapien
6	40	100.0	82	4	Q16014	Q16014 homo sapien
7	40	100.0	82	4	Q16019	Q16019 homo sapien
8	40	100.0	113	13	Q8JH58	Q8jh58 chelydra se
9	40	100.0	218	11	Q8BPV5	Q8bpv5 mus musculu
10	40	100.0	357	13	Q8UUI8	Q8uui8 brachydanio
11	40	100.0	384	11	Q8BPC7	Q8bpc7 mus musculu
12	40	100.0	472	13	Q8UUS0	Q8uus0 brachydanio
13	40	100.0	534	13	O93296	O93296 gallus gall
14	40	100.0	569	13	Q9PVL1	Q9pvl1 gallus gall
15	40	100.0	612	13	Q9I9E7	Q9i9e7 brachydanio
16	40	100.0	678	13	Q7ZZT1	Q7zzt1 brachydanio
17	40	100.0	695	13	Q9DGJ8	Q9dgj8 gallus gall
18	40	100.0	738	13	Q90W28	Q90w28 brachydanio
19	40	100.0	751	13	Q9DGJ7	Q9dgj7 gallus gall
20	37	92.5	1676	16	Q8A6R7	Q8a6r7 bacteroides
21	36	90.0	693	13	Q98SG0	Q98sg0 xenopus lae
22	36	90.0	747	13	Q91963	Q91963 xenopus. ap
23	33	82.5	162	8	Q32406	Q32406 heteranther
24	33	82.5	197	16	Q7VR77	Q7vr77 candidatus
25	33	82.5	695	13	Q98SF9	Q98sf9 xenopus lae
26	33	82.5	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
27	32	80.0	182	16	Q9Z588	Q9z588 streptomyce
28	32	80.0	184	16	Q931V3	Q931v3 staphylococ
29	32	80.0	261	2	Q7X225	Q7x225 staphylococ
30	32	80.0	261	2	Q7WRM0	Q7wrm0 staphylococ
31	32	80.0	261	16	Q99V89	Q99v89 staphylococ
32	32	80.0	268	16	Q8NXD0	Q8nxd0 staphylococ
33	32	80.0	282	16	Q8CUH9	Q8cuh9 oceanobacil
34	32	80.0	472	13	Q10833	Q10833 xenopus lae
35	32	80.0	501	16	Q7UZT9	Q7uzt9 prochloroco
36	32	80.0	1105	5	Q9VX31	Q9vx31 drosophila
37	32	80.0	2613	5	Q9GYD1	Q9gyd1 leishmania
38	31	77.5	49	6	O97917	O97917 bos taurus
39	31	77.5	147	16	Q8A5K5	Q8a5k5 bacteroides
40	31	77.5	179	16	Q82JK4	Q82jk4 streptomyce
41	31	77.5	208	16	Q8ESR7	Q8esr7 oceanobacil
42	31	77.5	228	16	Q8E2V5	Q8e2v5 streptococc
43	31	77.5	228	16	Q8DX05	Q8dx05 streptococc
44	31	77.5	248	5	Q8I3W8	Q8i3w8 plasmodium
45	31	77.5	259	16	Q8NN32	Q8nn32 corynebacte

ALIGNMENTS

RESULT 1
Q9UCD1
ID   Q9UCD1   PRELIMINARY;   PRT;   28 AA.
AC   Q9UCD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```
DE      Beta-amyloid peptide (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=94045685; PubMed=8229004;
RA      Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT      "Characterization of beta-amyloid peptide from human cerebrospinal
RT      fluid.";
RL      J. Neurochem. 61:1965-1968(1993).
DR      HSSP; P05067; 1AMB.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF03494; Beta-APP; 1.
SQ      SEQUENCE    28 AA;   3244 MW;   DE7BD081160AFC81 CRC64;

   Query Match                 100.0%;   Score 40;   DB 4;   Length 28;
   Best Local Similarity   100.0%;   Pred. No. 0.21;
   Matches     8;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy             1 KLVFFAED 8
                 ||||||||
Db            16 KLVFFAED 23


RESULT 2
Q9UCA9
ID      Q9UCA9         PRELIMINARY;        PRT;     30 AA.
AC      Q9UCA9;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Beta-amyloid protein (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=94153015; PubMed=8109908;
RA      Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT      "The amino acid sequence of neuritic plaque amyloid from a familial
RT      Alzheimer's disease patient.";
RL      Ann. Neurol. 35:245-246(1994).
DR      HSSP; P05067; 1BA4.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF03494; Beta-APP; 1.
SQ      SEQUENCE    30 AA;   3391 MW;   FF4167ABD081160A CRC64;

   Query Match                 100.0%;   Score 40;   DB 4;   Length 30;
   Best Local Similarity   100.0%;   Pred. No. 0.23;
   Matches     8;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy             1 KLVFFAED 8
```

```
                   | | | | | | | |
Db         16 KLVFFAED 23


RESULT 3
Q9UC33
ID   Q9UC33      PRELIMINARY;      PRT;    33 AA.
AC   Q9UC33;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93024877; PubMed=1406936;
RA   Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA   Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT   "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT   biological fluids.";
RL   Nature 359:325-327(1992).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   33 AA;  3674 MW;  B1DEFE2F4167ABD0 CRC64;

   Query Match            100.0%;  Score 40;  DB 4;  Length 33;
   Best Local Similarity  100.0%;  Pred. No. 0.25;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 KLVFFAED 8
                   | | | | | | | |
Db         16 KLVFFAED 23


RESULT 4
O35463
ID   O35463      PRELIMINARY;      PRT;    79 AA.
AC   O35463;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alzheimer's amyloid beta protein (Fragment).
GN   BETA APP.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sambamurti K., Pinnix I., Gandhi S.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
```

```
DR    EMBL; AF030413; AAB86608.1; -.
DR    HSSP; P05067; 1BA4.
DR    GO; GO:0016020; C:membrane; IEA.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF03494; Beta-APP; 1.
FT    NON_TER         1       1
FT    NON_TER        79      79
SQ    SEQUENCE   79 AA;   8538 MW;   37F2C6C3BFF3F597 CRC64;

   Query Match              100.0%;   Score 40;   DB 11;   Length 79;
   Best Local Similarity    100.0%;   Pred. No. 0.58;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy            1 KLVFFAED 8
                ||||||||
Db           36 KLVFFAED 43




RESULT 5
Q16020
ID    Q16020       PRELIMINARY;       PRT;      82 AA.
AC    Q16020;
DT    01-NOV-1996 (TrEMBLrel. 01, Created)
DT    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE    Beta-amyloid peptide (Fragment).
GN    BETA APP.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=93236601; PubMed=8476439;
RA    Denman R.B., Rosenzcwaig R., Miller D.L.;
RT    "A system for studying the effect(s) of familial Alzheimer disease
RT    mutations on the processing of the beta-amyloid peptide precursor.";
RL    Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR    EMBL; S61383; AAB26265.2; -.
DR    HSSP; P05067; 1BA4.
DR    GO; GO:0016020; C:membrane; IEA.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF03494; Beta-APP; 1.
FT    NON_TER         1       1
FT    NON_TER        82      82
SQ    SEQUENCE   82 AA;   8882 MW;   F534AA5AE5D9230A CRC64;

   Query Match              100.0%;   Score 40;   DB 4;   Length 82;
   Best Local Similarity    100.0%;   Pred. No. 0.61;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 KLVFFAED 8
                ||||||||
Db           33 KLVFFAED 40


RESULT 6
```

Q16014
ID   Q16014   PRELIMINARY;   PRT;   82 AA.
AC   Q16014;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S60721; AAB26263.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER   1   1
FT   NON_TER   82   82
SQ   SEQUENCE   82 AA;   8972 MW;   F534AA5B3EA9230A CRC64;

  Query Match   100.0%;   Score 40;   DB 4;   Length 82;
  Best Local Similarity   100.0%;   Pred. No. 0.61;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   33 KLVFFAED 40

RESULT 7
Q16019
ID   Q16019   PRELIMINARY;   PRT;   82 AA.
AC   Q16019;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61380; AAB26264.2; -.

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DR    HSSP; P05067; 1BA4.
DR    GO; GO:0016020; C:membrane; IEA.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF03494; Beta-APP; 1.
FT    NON_TER          1        1
FT    NON_TER         82       82
SQ    SEQUENCE    82 AA;   8938 MW;   F534AA50E579230A CRC64;

   Query Match                 100.0%;  Score 40;  DB 4;  Length 82;
   Best Local Similarity    100.0%;  Pred. No. 0.61;
   Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy            1 KLVFFAED 8
                |||||||||
Db           33 KLVFFAED 40



RESULT 8
Q8JH58
ID    Q8JH58        PRELIMINARY;        PRT;    113 AA.
AC    Q8JH58;
DT    01-OCT-2002 (TrEMBLrel. 22, Created)
DT    01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE    Amyloid beta protein (Fragment).
OS    Chelydra serpentina serpentina (common snapping turtle).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX    NCBI_TaxID=134619;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=21876906; PubMed=11882478;
RA    Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT    "Octylphenol (OP) alters the expression of members of the amyloid
RT    protein family in the hypothalamus of the snapping turtle, Chelydra
RT    serpentina serpentina.";
RL    Environ. Health Perspect. 110:269-275(2002).
DR    EMBL; AF541917; AAN04908.1; -.
DR    GO; GO:0016020; C:membrane; IEA.
DR    InterPro; IPR008155; A4_APP.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF03494; Beta-APP; 1.
DR    PRINTS; PR00203; AMYLOIDA4.
DR    PROSITE; PS00320; A4_INTRA; 1.
FT    NON_TER          1        1
SQ    SEQUENCE    113 AA;   12750 MW;   72515C930496E053 CRC64;

   Query Match                 100.0%;  Score 40;  DB 13;  Length 113;
   Best Local Similarity    100.0%;  Pred. No. 0.83;
   Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 KLVFFAED 8
                |||||||||
Db           30 KLVFFAED 37



RESULT 9
```

```
Q8BPV5
ID   Q8BPV5       PRELIMINARY;       PRT;    218 AA.
AC   Q8BPV5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid beta (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK052448; BAC34997.1; -.
DR   MGD; MGI:88059; App.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER         1        1
SQ   SEQUENCE   218 AA;   24118 MW;   95B55AFDAE1D0EF5 CRC64;

   Query Match              100.0%;  Score 40;  DB 11;  Length 218;
   Best Local Similarity    100.0%;  Pred. No. 1.6;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 KLVFFAED 8
              | | | | | | | |
Db        135 KLVFFAED 142




RESULT 10
Q8UUI8
ID   Q8UUI8       PRELIMINARY;       PRT;    357 AA.
AC   Q8UUI8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative mebrane protein (Fragment).
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   TISSUE=Embryo;
RX   PubMed=11862463;
RA   Musa A., Lehrach H., Russo V.E.A.;
RT   "Distinct expression patterns of two zebrafish homologues of the human
RT   APP gene during embryonic development.";
RL   Dev. Genes Evol. 211:563-567(2001).
DR   EMBL; AJ315637; CAC85734.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER         1         1
SQ   SEQUENCE   357 AA;   40962 MW;   07D99EEF6C55B2D8 CRC64;

   Query Match                 100.0%;   Score 40;   DB 13;   Length 357;
   Best Local Similarity   100.0%;   Pred. No. 2.6;
   Matches     8;   Conservative   0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        274 KLVFFAED 281


RESULT 11
Q8BPC7
ID   Q8BPC7         PRELIMINARY;       PRT;    384 AA.
AC   Q8BPC7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid beta (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK076506; BAC36369.1; -.
DR   MGD; MGI:88059; App.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER         1         1
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SQ   SEQUENCE   384 AA;   43990 MW;   A81B1AD8AE683173 CRC64;

   Query Match                 100.0%;   Score 40;   DB 11;   Length 384;
   Best Local Similarity   100.0%;   Pred. No. 2.8;
   Matches     8;   Conservative     0;   Mismatches     0;   Indels     0;   Gaps     0;

Qy          1 KLVFFAED 8
              ||||||||
Db        301 KLVFFAED 308


RESULT 12
Q8UUS0
ID   Q8UUS0        PRELIMINARY;        PRT;    472 AA.
AC   Q8UUS0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative membrane protein (Fragment).
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11862463;
RA   Musa A., Lehrach H., Russo V.E.A.;
RT   "Distinct expression patterns of two zebrafish homologues of the human
RT   APP gene during embryonic development.";
RL   Dev. Genes Evol. 211:563-567(2001).
DR   EMBL; AJ315636; CAC85733.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER        1        1
SQ   SEQUENCE    472 AA;   53787 MW;   24F7128BE3356550 CRC64;

   Query Match                 100.0%;   Score 40;   DB 13;   Length 472;
   Best Local Similarity   100.0%;   Pred. No. 3.4;
   Matches     8;   Conservative     0;   Mismatches     0;   Indels     0;   Gaps     0;

Qy          1 KLVFFAED 8
              ||||||||
Db        389 KLVFFAED 396


RESULT 13
O93296
ID   O93296        PRELIMINARY;        PRT;    534 AA.
AC   O93296;
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DT     01-NOV-1998 (TrEMBLrel. 08, Created)
DT     01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT     01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE     Amyloid protein (Fragment).
OS     Gallus gallus (Chicken).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC     Gallus.
OX     NCBI_TaxID=9031;
RN     [1]
RP     SEQUENCE FROM N.A.
RX     MEDLINE=98337885; PubMed=9671674;
RA     Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA     Milligan C.E.;
RT     "Increased production of amyloid precursor protein provides a
RT     substrate for caspase-3 in dying motoneurons.";
RL     J. Neurosci. 18:5869-5880(1998).
DR     EMBL; AF042098; AAC25052.1; -.
DR     HSSP; P05067; 1BA4.
DR     GO; GO:0016020; C:membrane; IEA.
DR     InterPro; IPR008155; A4_APP.
DR     InterPro; IPR008154; A4_extra.
DR     InterPro; IPR001255; Beta-APP.
DR     Pfam; PF02177; A4_EXTRA; 1.
DR     Pfam; PF03494; Beta-APP; 1.
DR     PRINTS; PR00203; AMYLOIDA4.
DR     PROSITE; PS00319; A4_EXTRA; 1.
DR     PROSITE; PS00320; A4_INTRA; 1.
FT     NON_TER         1        1
SQ     SEQUENCE    534 AA;   60597 MW;   FB53ECC2E66D4C92 CRC64;

   Query Match               100.0%;  Score 40;  DB 13;   Length 534;
   Best Local Similarity     100.0%;  Pred. No. 3.8;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
               ||||||||
Db        451 KLVFFAED 458


RESULT 14
Q9PVL1
ID     Q9PVL1       PRELIMINARY;       PRT;    569 AA.
AC     Q9PVL1;
DT     01-MAY-2000 (TrEMBLrel. 13, Created)
DT     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT     01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE     Amyloid protein (Fragment).
GN     APP.
OS     Gallus gallus (Chicken).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC     Gallus.
OX     NCBI_TaxID=9031;
RN     [1]
RP     SEQUENCE FROM N.A.
RC     TISSUE=Brain;
```

```
RA    Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT    "What the evolution of the amyloid protein precursor supergene family
RT    tells us about its function.";
RL    Neurochem. Int. 0:0-0(2000).
DR    EMBL; AF030341; AAF12698.1; -.
DR    HSSP; P05067; 1BA4.
DR    GO; GO:0016020; C:membrane; IEA.
DR    InterPro; IPR008155; A4_APP.
DR    InterPro; IPR008154; A4_extra.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF02177; A4_EXTRA; 1.
DR    Pfam; PF03494; Beta-APP; 1.
DR    PRINTS; PR00203; AMYLOIDA4.
DR    PROSITE; PS00319; A4_EXTRA; 1.
DR    PROSITE; PS00320; A4_INTRA; 1.
FT    NON_TER        1        1
SQ    SEQUENCE   569 AA;   64753 MW;   0AB8BB851863A19D CRC64;

   Query Match                 100.0%;   Score 40;   DB 13;   Length 569;
   Best Local Similarity   100.0%;   Pred. No. 4.1;
   Matches     8;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        487 KLVFFAED 494


RESULT 15
Q9I9E7
ID    Q9I9E7        PRELIMINARY;       PRT;    612 AA.
AC    Q9I9E7;
DT    01-OCT-2000 (TrEMBLrel. 15, Created)
DT    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE    Amyloid protein (Fragment).
GN    APPA.
OS    Brachydanio rerio (Zebrafish) (Danio rerio).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC    Cyprinidae; Danio.
OX    NCBI_TaxID=7955;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Slavov D.B., Gardiner K.;
RT    "An App cDNA from Zebrafish (Danio rerio).";
RL    Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AF257742; AAF71748.1; -.
DR    HSSP; P05067; 1HZ3.
DR    ZFIN; ZDB-GENE-000616-13; appa.
DR    GO; GO:0016020; C:membrane; IEA.
DR    InterPro; IPR008155; A4_APP.
DR    InterPro; IPR008154; A4_extra.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF02177; A4_EXTRA; 1.
DR    Pfam; PF03494; Beta-APP; 1.
DR    PRINTS; PR00203; AMYLOIDA4.
DR    PROSITE; PS00319; A4_EXTRA; 1.
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DR    PROSITE; PS00320; A4_INTRA; 1.
FT    NON_TER          1        1
SQ    SEQUENCE    612 AA;   69710 MW;   59A9ACBDF9C59EFF CRC64;

  Query Match                100.0%;  Score 40;  DB 13;   Length 612;
  Best Local Similarity      100.0%;  Pred. No. 4.4;
  Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              | | | | | | | |
Db        529 KLVFFAED 536


Search completed: March  4, 2004, 15:38:54
Job time : 2.14894 secs
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                      GenCore version 5.1.6
                       Copyright (c) 1993 - 2004  Compugen Ltd.


OM protein - protein search, using sw model

Run on:          March  4, 2004, 15:22:30 ; Search time 0.255319 Seconds
                                            (without alignments)
                                            1631.532 Million cell updates/sec


Title:           US-09-668-314C-73
Perfect score:   40
Sequence:        1 KLVFFAED 8


Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5


Searched:        141681 seqs, 52070155 residues


Total number of hits satisfying chosen parameters:       141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       SwissProt_42:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                              SUMMARIES
                       %
                     Query
Result           Query
   No.    Score   Match Length DB   ID                      Description
------------------------------------------------------------------------------
       1      40   100.0     57   1   A4_URSMA                Q29149 ursus marit
       2      40   100.0     58   1   A4_CANFA                Q28280 canis famil
       3      40   100.0     58   1   A4_RABIT                Q28748 oryctolagus
       4      40   100.0     58   1   A4_SHEEP                Q28757 ovis aries
       5      40   100.0     59   1   A4_BOVIN                Q28053 bos taurus
       6      40   100.0    751   1   A4_SAISC                Q95241 s amyloid b
       7      40   100.0    770   1   A4_CAVPO                Q60495 c amyloid b
       8      40   100.0    770   1   A4_HUMAN                P05067 h amyloid b
       9      40   100.0    770   1   A4_MACFA                P53601 m amyloid b
      10      40   100.0    770   1   A4_MOUSE                P12023 m amyloid b
      11      40   100.0    770   1   A4_PIG                  P79307 s amyloid b
      12      40   100.0    770   1   A4_RAT                  P08592 r amyloid b
      13      40   100.0    780   1   A4_TETFL                O73683 tetraodon f
      14      37    92.5    737   1   A4_FUGRU                O93279 fugu rubrip
      15      34    85.0    321   1   Y189_RICPR              Q9zdx5 rickettsia
      16      31    77.5    119   1   RL7A_ARCFU              O29494 archaeoglob
      17      31    77.5    281   1   UPK_CORST               Q9fb58 corynebacte
      18      31    77.5    641   1   LICR_BACSU              P46321 bacillus su
```

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19      31      77.5    2196    1   MOR2_SCHPO              Q9hdv6  schizosacch
20      30      75.0     214    1   UT11_ORYSA              Q8s1z1  oryza sativ
21      30      75.0     341    1   Y665_METJA              Q58079  methanococc
22      30      75.0     370    1   GP85_HUMAN              Q9npd1  homo sapien
23      30      75.0     371    1   GP85_BRARE              Q9i919  brachydanio
24      30      75.0     533    1   SYK_METMP               O30522  methanococc
25      30      75.0    1353    1   CYA9_HUMAN              O60503  homo sapien
26      30      75.0    1353    1   CYA9_MOUSE              P51830  mus musculu
27      29      72.5     119    1   RL7A_HALMA              P12743  haloarcula
28      29      72.5     189    1   CME2_BACSU              P32393  bacillus su
29      29      72.5     258    1   RSFA_BACSU              P39650  bacillus su
30      29      72.5     278    1   ERA_BUCAP               Q8k9r2  buchnera ap
31      29      72.5     286    1   DMA_HAEIN               P44431  haemophilus
32      29      72.5     357    1   HST2_YEAST              P53686  saccharomyc
33      29      72.5     469    1   RECJ_METJA              Q58387  methanococc
34      29      72.5     481    1   RNF9_PANTR              Q7yr32  pan troglod
35      29      72.5     482    1   RNF9_HUMAN              Q9udy6  homo sapien
36      29      72.5     634    1   ELM1_ASPFU              P46074  aspergillus
37      29      72.5     634    1   ELM2_ASPFU              P46075  aspergillus
38      29      72.5     809    1   KCB2_CANFA              Q95167  canis famil
39      29      72.5     857    1   KCB1_MOUSE              Q03717  mus musculu
40      29      72.5     857    1   KCB1_RAT                P15387  rattus norv
41      29      72.5     858    1   KCB1_HUMAN              Q14721  homo sapien
42      29      72.5     858    1   KCB1_PIG                O18868  sus scrofa
43      29      72.5     858    1   KCB1_RABIT              Q9mz19  oryctolagus
44      29      72.5     907    1   KCB2_RAT                Q63099  rattus norv
45      29      72.5     911    1   KCB2_HUMAN              Q92953  homo sapien
```

ALIGNMENTS

RESULT 1
A4_URSMA
ID   A4_URSMA   STANDARD;   PRT;   57 AA.
AC   Q29149;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX   NCBI_TaxID=29073;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC   intracellular signaling pathway through the GTP-binding protein

```
CC         G(O) (By similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    -!- SIMILARITY: Belongs to the APP family.
CC    ------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC    the European Bioinformatics Institute.  There are no  restrictions on  its
CC    use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    ------------------------------------------------------------------
DR    EMBL; X56128; CAA39593.1; -.
DR    PIR; B60045; B60045.
DR    HSSP; P05067; 1BA4.
DR    InterPro; IPR008155; A4_APP.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF03494; Beta-APP; 1.
DR    PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR    PROSITE; PS00320; A4_INTRA; PARTIAL.
KW    Glycoprotein; Amyloid; Neurone; Transmembrane.
FT    NON_TER        1      1
FT    CHAIN          6      48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT    DOMAIN        <1      33       EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM      34      57       POTENTIAL.
FT    NON_TER       57      57
SQ    SEQUENCE     57 AA;   6172 MW;   84209D88EBA82DFA CRC64;

   Query Match              100.0%;   Score 40;   DB 1;   Length 57;
   Best Local Similarity    100.0%;   Pred. No.  0.029;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 2
A4_CANFA
ID    A4_CANFA        STANDARD;      PRT;     58 AA.
AC    Q28280;
DT    01-NOV-1997 (Rel. 35, Created)
DT    01-NOV-1997 (Rel. 35, Last sequence update)
DT    30-MAY-2000 (Rel. 39, Last annotation update)
DE    Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE    protein (Beta-APP) (A-beta)] (Fragment).
GN    APP.
OS    Canis familiaris (Dog).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX    NCBI_TaxID=9615;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Kidney;
RX    MEDLINE=92017079; PubMed=1656157;
RA    Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT    "Conservation of the sequence of the Alzheimer's disease amyloid
```

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RT    peptide in dog, polar bear and five other mammals by cross-species
RT    polymerase chain reaction analysis.";
RL    Brain Res. Mol. Brain Res. 10:299-305(1991).
CC    -!- FUNCTION: Functional neuronal receptor which couples to
CC        intracellular signaling pathway through the GTP-binding protein
CC        G(O) (By similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    -!- SIMILARITY: Belongs to the APP family.
CC    ------------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC    use  by  non-profit  institutions as long  as its content  is  in  no  way
CC    modified and this statement is not removed.  Usage  by  and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    ------------------------------------------------------------------------
DR    EMBL; X56125; CAA39590.1; -.
DR    HSSP; P05067; 1BA4.
DR    InterPro; IPR008155; A4_APP.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF03494; Beta-APP; 1.
DR    PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR    PROSITE; PS00320; A4_INTRA; PARTIAL.
KW    Glycoprotein; Amyloid; Neurone; Transmembrane.
FT    NON_TER         1       1
FT    CHAIN           7      49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT    DOMAIN         <1      34       EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM       35      58       POTENTIAL.
FT    NON_TER        58      58
SQ    SEQUENCE    58 AA;  6285 MW;  8469D488A2E12DFA CRC64;

   Query Match              100.0%;  Score 40;  DB 1;  Length 58;
   Best Local Similarity    100.0%;  Pred. No. 0.03;
   Matches     8;  Conservative    0;  Mismatches     0;  Indels     0;  Gaps     0;

Qy            1 KLVFFAED 8
                ||||||||
Db           22 KLVFFAED 29


RESULT 3
A4_RABIT
ID    A4_RABIT        STANDARD;       PRT;      58 AA.
AC    Q28748;
DT    01-NOV-1997 (Rel. 35, Created)
DT    01-NOV-1997 (Rel. 35, Last sequence update)
DT    16-OCT-2001 (Rel. 40, Last annotation update)
DE    Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE    protein (Beta-APP) (A-beta)] (Fragment).
GN    APP.
OS    Oryctolagus cuniculus (Rabbit).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX    NCBI_TaxID=9986;
RN    [1]
RP    SEQUENCE FROM N.A.
```

```
RC    TISSUE=Brain;
RX    MEDLINE=92017079; PubMed=1656157;
RA    Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT    "Conservation of the sequence of the Alzheimer's disease amyloid
RT    peptide in dog, polar bear and five other mammals by cross-species
RT    polymerase chain reaction analysis.";
RL    Brain Res. Mol. Brain Res. 10:299-305(1991).
CC    -!- FUNCTION: Functional neuronal receptor which couples to
CC        intracellular signaling pathway through the GTP-binding protein
CC        G(O) (By similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    -!- SIMILARITY: Belongs to the APP family.
CC    ------------------------------------------------------------------------
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CC    or send an email to license@isb-sib.ch).
CC    ------------------------------------------------------------------------
DR    EMBL; X56129; CAA39594.1; -.
DR    HSSP; P05067; 1BA4.
DR    InterPro; IPR008155; A4_APP.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF03494; Beta-APP; 1.
DR    PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR    PROSITE; PS00320; A4_INTRA; PARTIAL.
KW    Glycoprotein; Amyloid; Neurone; Transmembrane.
FT    NON_TER          1       1
FT    CHAIN            6      48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT    DOMAIN          <1      33       EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM        34      57       POTENTIAL.
FT    DOMAIN          58     >58       CYTOPLASMIC (POTENTIAL).
FT    NON_TER         58      58
SQ    SEQUENCE    58 AA;   6300 MW;   F434209D88EBA82D CRC64;

   Query Match                100.0%;   Score 40;   DB 1;   Length 58;
   Best Local Similarity      100.0%;   Pred. No. 0.03;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 4
A4_SHEEP
ID    A4_SHEEP        STANDARD;      PRT;      58 AA.
AC    Q28757;
DT    01-NOV-1997 (Rel. 35, Created)
DT    01-NOV-1997 (Rel. 35, Last sequence update)
DT    30-MAY-2000 (Rel. 39, Last annotation update)
DE    Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE    protein (Beta-APP) (A-beta)] (Fragment).
GN    APP.
OS    Ovis aries (Sheep).
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OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC    Bovidae; Caprinae; Ovis.
OX    NCBI_TaxID=9940;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Heart;
RX    MEDLINE=92017079; PubMed=1656157;
RA    Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT    "Conservation of the sequence of the Alzheimer's disease amyloid
RT    peptide in dog, polar bear and five other mammals by cross-species
RT    polymerase chain reaction analysis.";
RL    Brain Res. Mol. Brain Res. 10:299-305(1991).
CC    -!- FUNCTION: Functional neuronal receptor which couples to
CC        intracellular signaling pathway through the GTP-binding protein
CC        G(O) (By similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    -!- SIMILARITY: Belongs to the APP family.
CC    --------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------
DR    EMBL; X56130; CAA39595.1; -.
DR    HSSP; P05067; 1BA4.
DR    InterPro; IPR008155; A4_APP.
DR    InterPro; IPR001255; Beta-APP.
DR    Pfam; PF03494; Beta-APP; 1.
DR    PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR    PROSITE; PS00320; A4_INTRA; PARTIAL.
KW    Glycoprotein; Amyloid; Neurone; Transmembrane.
FT    NON_TER        1       1
FT    CHAIN          6      48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT    DOMAIN        <1      33       EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM      34      57       POTENTIAL.
FT    DOMAIN        58     >58       CYTOPLASMIC (POTENTIAL).
FT    NON_TER       58      58
SQ    SEQUENCE     58 AA;   6300 MW;   F434209D88EBA82D CRC64;

   Query Match              100.0%;  Score 40;  DB 1;   Length 58;
   Best Local Similarity    100.0%;  Pred. No. 0.03;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 5
A4_BOVIN
ID    A4_BOVIN        STANDARD;      PRT;     59 AA.
AC    Q28053;
DT    01-NOV-1997 (Rel. 35, Created)
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DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC   intracellular signaling pathway through the GTP-binding protein
CC   G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER   1   1
FT   CHAIN   7   49   BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN   <1   34   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   35   58   POTENTIAL.
FT   DOMAIN   59   >59   CYTOPLASMIC (POTENTIAL).
FT   NON_TER   59   59
SQ   SEQUENCE   59 AA;   6414 MW;   F43469D488A2E12D CRC64;

     Query Match   100.0%; Score 40; DB 1; Length 59;
     Best Local Similarity   100.0%; Pred. No. 0.03;
     Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              | | | | | | | |
Db   22 KLVFFAED 29

RESULT 6
A4_SAISC
ID   A4_SAISC   STANDARD;   PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC   physiological functions on the surface of neurons relevant to
CC   neurite growth, neuronal adhesion and axonogenesis. Involved in
CC   cell mobility and transcription regulation through protein-protein
CC   interactions (By similarity). Can promote transcription activation
CC   through binding to APBB1/Tip60 and inhibit Notch signaling through
CC   interaction with Numb (By similarity). Couples to apoptosis-
CC   inducing pathways such as those mediated by G(O) and JIP (By
CC   similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC   Acts as a kinesin I membrane receptor, mediating the axonal
CC   transport of beta-secretase and presenilin 1 (By similarity). May
CC   be involved in copper homeostasis/oxidative stress through copper
CC   ion reduction. In vitro, copper-metallated APP induces neuronal
CC   death directly or is potentiated through Cu(II)-mediated low-
CC   density lipoprotein oxidation (By similarity). Can regulate
CC   neurite outgrowth through binding to components of the
CC   extracellular matrix such as heparin and collagen I and IV (By
CC   similarity). The splice isoforms that contain the BPTI domain
CC   possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC   with metal-reducing activity. Bind transient metals such as
CC   copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC   peptides, including C31, are potent enhancers of neuronal
CC   apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC   cytoplasmic proteins, including APBB family members, the APBA
CC   family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding

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CC          to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC          interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC          (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC          In vitro, it binds MAPT via the MT-binding domains (By
CC          similarity). Associates with microtubules in the presence of ATP
CC          and in a kinesin-dependent manner (By similarity).
CC     -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC          protein that rapidly becomes internalized via clathrin-coated
CC          pits. During maturation, the immature APP (N-glycosylated in the
CC          endoplasmic reticulum) moves to the Golgi complex where complete
CC          maturation occurs (O-glycosylated and sulfated). After alpha-
CC          secretase cleavage, soluble APP is released into the extracellular
CC          space and the C-terminal is internalized to endosomes and
CC          lysosomes. Some APP accumulates in secretory transport vesicles
CC          leaving the late Golgi compartment and returns to the cell
CC          surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC          and nuclei of neurons (By similarity).
CC     -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=2;
CC            Comment=Additional isoforms seem to exist;
CC          Name=APP770;
CC            IsoId=Q95241-1; Sequence=Displayed;
CC          Name=APP695;
CC            IsoId=Q95241-2; Sequence=Not described;
CC     -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC          sorting of membrane proteins to the basolateral surface of
CC          epithelial cells (By similarity).
CC     -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC          phosphorylated proteins is required for the specific binding of
CC          the PID domain. However additional amino acids either N- or C-
CC          terminal to the NPXY motif are often required for complete
CC          interaction. The PID domain-containing proteins which bind APP
CC          require the YENPTY motif for full interaction. These interactions
CC          are independent of phosphorylation on the terminal tyrosine
CC          residue. The NPXY site is also involved in clathrin-mediated
CC          endocytosis (By similarity).
CC     -!- PTM: Proteolytically processed under normal cellular conditions.
CC          Cleavage by alpha-secretase or alternatively by beta-secretase
CC          leads to generation and extracellular release of soluble APP
CC          peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC          retention of corresponding membrane-anchored C-terminal fragments,
CC          C83 and C99. Subsequent processing of C83 by gamma-secretase
CC          yields P3 peptides. This is the major secretory pathway and is
CC          nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC          gamma-secretase processing of C99 releases the amyloid beta
CC          proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC          major components of amyloid plaques, and the cytotoxic C-terminal
CC          fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC          similarity).
CC     -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC          (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC          results in the production of the neurotoxic C31 peptide and the
CC          increased production of beta-amyloid peptides (By similarity).
CC     -!- PTM: N- and O-glycosylated (By similarity).
CC     -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC          serine residues is neuron-specific. Phosphorylation can affect APP
CC          processing, neuronal differentiation and interaction with other
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CC          proteins (By similarity).
CC     -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC          zinc, can induce histidine-bridging between beta-amyloid molecules
CC          resulting in beta-amyloid-metal aggregates (By similarity).
CC          Extracellular zinc-binding increases binding of heparin to APP and
CC          inhibits collagen-binding (By similarity).
CC     -!- SIMILARITY: Belongs to the APP family.
CC     -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC     ------------------------------------------------------------------------
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CC     or send an email to license@isb-sib.ch).
CC     ------------------------------------------------------------------------
DR     EMBL; S81024; AAD14347.1; -.
DR     HSSP; P05067; 1AAP.
DR     InterPro; IPR008155; A4_APP.
DR     InterPro; IPR008154; A4_extra.
DR     InterPro; IPR001255; Beta-APP.
DR     InterPro; IPR002223; Kunitz_BPTI.
DR     Pfam; PF02177; A4_EXTRA; 1.
DR     Pfam; PF03494; Beta-APP; 1.
DR     Pfam; PF00014; Kunitz_BPTI; 1.
DR     PRINTS; PR00203; AMYLOIDA4.
DR     PRINTS; PR00759; BASICPTASE.
DR     ProDom; PD000222; Kunitz_BPTI; 1.
DR     SMART; SM00006; A4_EXTRA; 1.
DR     SMART; SM00131; KU; 1.
DR     PROSITE; PS00319; A4_EXTRA; 1.
DR     PROSITE; PS00320; A4_INTRA; 1.
DR     PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR     PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW     Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW     Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW     Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW     Proteoglycan; Amyloid; Alternative splicing.
FT     SIGNAL          1      17          BY SIMILARITY.
FT     CHAIN          18     751          A4 PROTEIN.
FT     CHAIN          18     668          SOLUBLE APP-ALPHA (POTENTIAL).
FT     CHAIN          18     652          SOLUBLE APP-BETA (POTENTIAL).
FT     CHAIN         653     751          C99 (POTENTIAL).
FT     CHAIN         653     694          BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT     CHAIN         653     692          BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT     CHAIN         669     751          C83 (POTENTIAL).
FT     CHAIN         669     694          P3(42) (POTENTIAL).
FT     CHAIN         669     692          P3(40) (POTENTIAL).
FT     CHAIN         693     751          GAMMA-CTF(59) (POTENTIAL).
FT     CHAIN         695     751          GAMMA-CTF(57) (POTENTIAL).
FT     CHAIN         702     751          GAMMA-CTF(50) (POTENTIAL).
FT     CHAIN         721     751          C31 (POTENTIAL).
FT     DOMAIN         18     680          EXTRACELLULAR (POTENTIAL).
FT     TRANSMEM      681     704          POTENTIAL.
FT     DOMAIN        705     751          CYTOPLASMIC (POTENTIAL).
FT     DOMAIN         96     110          HEPARIN-BINDING (BY SIMILARITY).
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FT   DOMAIN       181   188   ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN       291   341   BPTI/KUNITZ INHIBITOR.
FT   DOMAIN       316   344   HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       363   428   HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       504   521   COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN       713   732   INTERACTION WITH G(O)-ALPHA
FT                            (BY SIMILARITY).
FT   DOMAIN       230   260   ASP/GLU-RICH (ACIDIC).
FT   DOMAIN       274   280   POLY-THR.
FT   SITE         144   144   REQUIRED FOR COPPER(II) REDUCTION
FT                            (BY SIMILARITY).
FT   ACT_SITE     301   302   REACTIVE BOND.
FT   SITE         652   653   CLEAVAGE (BY BETA-SECRETASE)
FT                            (BY SIMILARITY).
FT   SITE         653   654   CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE         668   669   CLEAVAGE (BY ALPHA-SECRETASE)
FT                            (BY SIMILARITY).
FT   SITE         685   685   INVOLVED IN FREE RADICAL PROPAGATION
FT                            (BY SIMILARITY).
FT   SITE         687   687   INVOLVED IN OXIDATIVE REACTIONS
FT                            (BY SIMILARITY).
FT   SITE         692   693   CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                            (BY SIMILARITY).
FT   SITE         694   695   CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                            (BY SIMILARITY).
FT   SITE         701   702   CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                            (BY SIMILARITY).
FT   SITE         705   715   BASOLATERAL SORTING SIGNAL
FT                            (BY SIMILARITY).
FT   SITE         720   721   CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                            (BY SIMILARITY).
FT   SITE         738   741   ENDOCYTOSIS SIGNAL.
FT   SITE         740   743   NPXY MOTIF.

   Query Match                100.0%;  Score 40;  DB 1;  Length 751;
   Best Local Similarity      100.0%;  Pred. No. 0.37;
   Matches     8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         1 KLVFFAED 8
             ||||||||
Db       668 KLVFFAED 675


RESULT 7
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
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OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
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CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
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CC          are independent of phosphorylation on the terminal tyrosine
CC          residue (By similarity). The NPXY site is also involved in
CC          clathrin-mediated endocytosis.
CC     -!- PTM: Proteolytically processed under normal cellular conditions.
CC          Cleavage by alpha-secretase or alternatively by beta-secretase
CC          leads to generation and extracellular release of soluble APP
CC          peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC          retention of corresponding membrane-anchored C-terminal fragments,
CC          CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC          gamma-secretase yields P3 peptides. This is the major secretory
CC          pathway and is nonamyloidogenic. Alternatively,
CC          presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC          beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC          and amyloid-beta 42 (Abeta42), major components of amyloid
CC          plaques, and the corresponding cytotoxic C-terminal fragments
CC          (CTFs).
CC     -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC          apoptosis (By similarity).
CC     -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC          the L-APP isoforms produces the APP proteoglycan core proteins,
CC          the appicans (By similarity).
CC     -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC          serine residues is neuron-specific (By similarity).
CC          Phosphorylation can affect APP processing, neuronal
CC          differentiation and interaction with other proteins.
CC     -!- PTM: Extracellular binding and reduction of copper, results in a
CC          corresponding oxidation of Cys-144 and Cys-158, and the formation
CC          of a disulfide bond (By similarity).
CC     -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC          zinc, can induce histidine-bridging between beta-amyloid molecules
CC          resulting in beta-amyloid-metal aggregates.
CC     -!- SIMILARITY: Belongs to the APP family.
CC     -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC     ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC     ------------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1      17       BY SIMILARITY.
FT   CHAIN        18     770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18     687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18     671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672     770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672     713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672     711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688     770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688     713       P3(42) (BY SIMILARITY).
FT   CHAIN       688     711       P3(40) (BY SIMILARITY).
FT   CHAIN       712     770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714     770       GAMMA-CTF(57) (BY SIMILARITY).
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   Query Match              100.0%;   Score 40;   DB 1;   Length 770;
   Best Local Similarity    100.0%;   Pred. No. 0.38;
   Matches     8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 KLVFFAED 8
              ||||||||
Db        687 KLVFFAED 694
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RESULT 8
A4_HUMAN
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ID   A4_HUMAN        STANDARD;       PRT;    770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC   Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
GN   APP OR A4 OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87144572; PubMed=2881207;
RA   Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA   Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT   "The precursor of Alzheimer's disease amyloid A4 protein resembles a
```

RT   cell-surface receptor.";
RL   Nature 325:733-736(1987).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM APP751).
RC   TISSUE=Brain;
RX   MEDLINE=88122639; PubMed=2893289;
RA   Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA   Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA   Cordell B.;
RT   "A new A4 amyloid mRNA contains a domain homologous to serine
RT   proteinase inhibitors.";
RL   Nature 331:525-527(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RX   MEDLINE=89128427; PubMed=2783775;
RA   Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA   Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT   "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT   is encoded by 16 exons.";
RL   Nucleic Acids Res. 17:517-522(1989).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP770).
RX   MEDLINE=90236318; PubMed=2110105;
RA   Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT   "Genomic organization of the human amyloid beta-protein precursor
RT   gene.";
RL   Gene 87:257-263(1990).
RN   [5]
RP   ERRATUM, AND REVISIONS.
RA   Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL   Gene 102:291-292(1991).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC   TISSUE=Leukocyte;
RX   MEDLINE=92268136; PubMed=1587857;
RA   Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA   Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT   "Identification and differential expression of a novel alternative
RT   splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT   leukocytes and brain microglial cells.";
RL   J. Biol. Chem. 267:10804-10809(1992).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM APP770).
RX   MEDLINE=97263807; PubMed=9108164;
RA   Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA   Saito M., Tsukuni S., Sakaki Y.;
RT   "A novel method for making nested deletions and its application for
RT   sequencing of a 300 kb region of human APP locus.";
RL   Nucleic Acids Res. 25:1802-1808(1997).
RN   [8]
RP   SEQUENCE FROM N.A. (ISOFORM APP639).
RC   TISSUE=Brain;
RX   MEDLINE=22744650; PubMed=12859342;
RA   Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT   "Identification of a novel alternative splicing isoform of human
RT   amyloid precursor protein gene, APP639.";
RL   Eur. J. Neurosci. 18:102-108(2003).

RN   [9]
RP   SEQUENCE FROM N.A. (ISOFORM APP305).
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [10]
RP   SEQUENCE OF 1-10 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89016647; PubMed=3140222;
RA   Schon E.A., Mita S., Sadlock J., Herbert J.;
RT   "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT   encodes a 95-kDa polypeptide.";
RL   Nucleic Acids Res. 16:9351-9351(1988).
RN   [11]
RP   ERRATUM, AND REVISIONS.
RA   Mita S., Sadlock J., Herbert J., Schon E.A.;
RL   Nucleic Acids Res. 16:11402-11402(1988).
RN   [12]
RP   SEQUENCE OF 1-75 FROM N.A.
RX   MEDLINE=89165870; PubMed=2538123;
RA   La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT   "Characterization of the 5'-end region and the first two exons of the
RT   beta-protein precursor gene.";
RL   Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN   [13]
RP   SEQUENCE OF 18-50.
RC   TISSUE=Fibroblast;
RX   MEDLINE=87250462; PubMed=3597385;
RA   van Nostrand W.E., Cunningham D.D.;
RT   "Purification of protease nexin II from human fibroblasts.";
RL   J. Biol. Chem. 262:8508-8514(1987).
RN   [14]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC   TISSUE=Brain;
RX   MEDLINE=89346754; PubMed=2569763;
RA   de Sauvage F., Octave J.N.;
RT   "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT   secreted protein.";

RL   Science 245:651-653(1989).
RN   [15]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87231971; PubMed=3035574;
RA   Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT   "Molecular cloning and characterization of a cDNA encoding the
RT   cerebrovascular and the neuritic plaque amyloid peptides.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN   [16]
RP   SEQUENCE OF 286-366 FROM N.A.
RX   MEDLINE=88122640; PubMed=2893290;
RA   Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA   Gusella J.F., Neve R.L.;
RT   "Protease inhibitor domain encoded by an amyloid protein precursor
RT   mRNA associated with Alzheimer's disease.";
RL   Nature 331:528-530(1988).
RN   [17]
RP   SEQUENCE OF 287-367 FROM N.A.
RX   MEDLINE=88122641; PubMed=2893291;
RA   Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT   "Novel precursor of Alzheimer's disease amyloid protein shows
RT   protease inhibitory activity.";
RL   Nature 331:530-532(1988).
RN   [18]
RP   SEQUENCE OF 507-770 FROM N.A.
RC   TISSUE=Brain cortex;
RX   MEDLINE=88124954; PubMed=2893379;
RA   Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA   Marotta C.A.;
RT   "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT   disease brain: coding and noncoding regions of the fetal precursor
RT   mRNA are expressed in the cortex.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN   [19]
RP   SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX   MEDLINE=96139497; PubMed=8576160;
RA   Beher D., Hesse L., Masters C.L., Multhaup G.;
RT   "Regulation of amyloid protein precursor (APP) binding to collagen and
RT   mapping of the binding sites on APP and collagen type I.";
RL   J. Biol. Chem. 271:1613-1620(1996).
RN   [20]
RP   SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP   AND AD GLY-717.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN   [21]
RP   SEQUENCE OF 656-737 FROM N.A.
RX   MEDLINE=89392030; PubMed=2675837;
RA   Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA   Little S.P.;
RT   "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT   similarity to soybean trypsin inhibitor.";
RL   Biochem. Biophys. Res. Commun. 163:1248-1255(1989).

RN   [22]

    Query Match   100.0%; Score 40; DB 1; Length 770;
    Best Local Similarity   100.0%; Pred. No. 0.38;
    Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              |||||||||
Db   687 KLVFFAED 694

RESULT 9
A4_MACFA
ID   A4_MACFA   STANDARD;   PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC   physiological functions on the surface of neurons relevant to
CC   neurite growth, neuronal adhesion and axonogenesis. Involved in
CC   cell mobility and transcription regulation through protein-protein
CC   interactions (By similarity). Can promote transcription activation
CC   through binding to APBB1/Tip60 and inhibit Notch signaling through
CC   interaction with Numb (By similarity). Couples to apoptosis-
CC   inducing pathways such as those mediated by G(O) and JIP (By
CC   similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC   Acts as a kinesin I membrane receptor, mediating the axonal
CC   transport of beta-secretase and presenilin 1 (By similarity). May
CC   be involved in copper homeostasis/oxidative stress through copper
CC   ion reduction. In vitro, copper-metallated APP induces neuronal
CC   death directly or is potentiated through Cu(II)-mediated low-
CC   density lipoprotein oxidation (By similarity). Can regulate
CC   neurite outgrowth through binding to components of the
CC   extracellular matrix such as heparin and collagen I and IV (By

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CC          similarity). The splice isoforms that contain the BPTI domain
CC          possess protease inhibitor activity (By similarity).
CC     -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC          with metal-reducing activity. Bind transient metals such as
CC          copper, zinc and iron (By similarity).
CC     -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC          peptides, including C31, are potent enhancers of neuronal
CC          apoptosis (By similarity).
CC     -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC          cytoplasmic proteins, including APBB family members, the APBA
CC          family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC          to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC          interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC          (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC          In vitro, it binds MAPT via the MT-binding domains (By
CC          similarity). Associates with microtubules in the presence of ATP
CC          and in a kinesin-dependent manner (By similarity).
CC     -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC          protein that rapidly becomes internalized via clathrin-coated
CC          pits. During maturation, the immature APP (N-glycosylated in the
CC          endoplasmic reticulum) moves to the Golgi complex where complete
CC          maturation occurs (O-glycosylated and sulfated). After alpha-
CC          secretase cleavage, soluble APP is released into the extracellular
CC          space and the C-terminal is internalized to endosomes and
CC          lysosomes. Some APP accumulates in secretory transport vesicles
CC          leaving the late Golgi compartment and returns to the cell
CC          surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC          and nuclei of neurons (By similarity).
CC     -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=2;
CC            Comment=Additional isoforms seem to exist;
CC          Name=APP770;
CC            IsoId=P53601-1; Sequence=Displayed;
CC          Name=APP695;
CC            IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC     -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC          sorting of membrane proteins to the basolateral surface of
CC          epithelial cells (By similarity).
CC     -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC          phosphorylated proteins is required for the specific binding of
CC          the PID domain. However additional amino acids either N- or C-
CC          terminal to the NPXY motif are often required for complete
CC          interaction. The PID domain-containing proteins which bind APP
CC          require the YENPTY motif for full interaction. These interactions
CC          are independent of phosphorylation on the terminal tyrosine
CC          residue. The NPXY site is also involved in clathrin-mediated
CC          endocytosis (By similarity).
CC     -!- PTM: Proteolytically processed under normal cellular conditions.
CC          Cleavage by alpha-secretase or alternatively by beta-secretase
CC          leads to generation and extracellular release of soluble APP
CC          peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC          retention of corresponding membrane-anchored C-terminal fragments,
CC          C83 and C99. Subsequent processing of C83 by gamma-secretase
CC          yields P3 peptides. This is the major secretory pathway and is
CC          nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC          gamma-secretase processing of C99 releases the amyloid beta
CC          proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
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CC          major components of amyloid plaques, and the cytotoxic C-terminal
CC          fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC          similarity).
CC       -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC          (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC          results in the production of the neurotoxic C31 peptide and the
CC          increased production of beta-amyloid peptides (By similarity).
CC       -!- PTM: N- and O-glycosylated (By similarity).
CC       -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC          serine residues is neuron-specific. Phosphorylation can affect APP
CC          processing, neuronal differentiation and interaction with other
CC          proteins (By similarity).
CC       -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC          zinc, can induce histidine-bridging between beta-amyloid molecules
CC          resulting in beta-amyloid-metal aggregates (By similarity).
CC          Extracellular zinc-binding increases binding of heparin to APP and
CC          inhibits collagen-binding (By similarity).
CC       -!- SIMILARITY: Belongs to the APP family.
CC       -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC       --------------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC       the European Bioinformatics Institute.  There are no  restrictions on  its
CC       use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC       or send an email to license@isb-sib.ch).
CC       --------------------------------------------------------------------------
DR       EMBL; M58727; AAA36829.1; -.
DR       EMBL; M58726; AAA36828.1; -.
DR       HSSP; P05067; 1AAP.
DR       InterPro; IPR008155; A4_APP.
DR       InterPro; IPR008154; A4_extra.
DR       InterPro; IPR001255; Beta-APP.
DR       InterPro; IPR002223; Kunitz_BPTI.
DR       Pfam; PF02177; A4_EXTRA; 1.
DR       Pfam; PF03494; Beta-APP; 1.
DR       Pfam; PF00014; Kunitz_BPTI; 1.
DR       PRINTS; PR00203; AMYLOIDA4.
DR       PRINTS; PR00759; BASICPTASE.
DR       ProDom; PD000222; Kunitz_BPTI; 1.
DR       SMART; SM00006; A4_EXTRA; 1.
DR       SMART; SM00131; KU; 1.
DR       PROSITE; PS00319; A4_EXTRA; 1.
DR       PROSITE; PS00320; A4_INTRA; 1.
DR       PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR       PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW       Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW       Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW       Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW       Proteoglycan; Alternative splicing; Amyloid.
FT       SIGNAL         1      17       BY SIMILARITY.
FT       CHAIN         18     770       AMYLOID BETA A4 PROTEIN.
FT       CHAIN         18     687       SOLUBLE APP-ALPHA (POTENTIAL).
FT       CHAIN         18     671       SOLUBLE APP-BETA (POTENTIAL).
FT       CHAIN        672     770       C99 (POTENTIAL).
FT       CHAIN        672     713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
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FT   CHAIN        672   711   BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN        688   770   C83 (POTENTIAL).
FT   CHAIN        688   713   P3(42) (POTENTIAL).
FT   CHAIN        688   711   P3(40) (POTENTIAL).
FT   CHAIN        712   770   GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN        714   770   GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN        721   770   GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN        740   770   C31 (POTENTIAL).
FT   DOMAIN        18   699   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     700   723   POTENTIAL.
FT   DOMAIN       724   770   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        96   110   HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       181   188   ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN       291   341   BPTI/KUNITZ INHIBITOR.
FT   DOMAIN       391   423   HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       491   522   HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       523   540   COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN       732   751   INTERACTION WITH G(O)-ALPHA
FT                            (BY SIMILARITY).
FT   DOMAIN       230   260   ASP/GLU-RICH (ACIDIC).
FT   DOMAIN       274   280   POLY-THR.
FT   SITE         144   144   REQUIRED FOR COPPER(II) REDUCTION
FT                            (BY SIMILARITY).
FT   ACT_SITE     301   302   REACTIVE BOND (BY SIMILARITY).
FT   SITE         671   672   CLEAVAGE (BY BETA-SECRETASE)
FT                            (BY SIMILARITY).
FT   SITE         672   673   CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE         687   688   CLEAVAGE (BY ALPHA-SECRETASE)
FT                            (BY SIMILARITY).
FT   SITE         704   704   IMPLICATED IN FREE RADICAL PROPAGATION
FT                            (BY SIMILARITY).
FT   SITE         706   706   INVOLVED IN OXIDATIVE REACTIONS
FT                            (BY SIMILARITY).
FT   SITE         711   712   CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                            (BY SIMILARITY).
FT   SITE         713   714   CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                            (BY SIMILARITY).
FT   SITE         720   721   CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                            (BY SIMILARITY).
FT   SITE         724   734   BASOLATERAL SORTING SIGNAL
FT                            (BY SIMILARITY).
FT   SITE         739   740   CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

     Query Match              100.0%;  Score 40;  DB 1;  Length 770;
     Best Local Similarity    100.0%;  Pred. No. 0.38;
     Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 KLVFFAED 8
               ||||||||
Db         687 KLVFFAED 694


RESULT 10
A4_MOUSE
ID   A4_MOUSE        STANDARD;      PRT;    770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
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DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   MEDLINE=21130647; PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;

RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Kidney;
RX   MEDLINE=89149813; PubMed=2493250;
RA   Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT   "Structure and expression of the alternatively-spliced forms of mRNA
RT   for the mouse homolog of Alzheimer's disease amyloid beta protein
RT   precursor.";
RL   Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN   [8]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   STRAIN=CD-1; TISSUE=Placenta;
RX   MEDLINE=89345111; PubMed=2569710;
RA   Fukuchi K., Martin G.M., Deeb S.S.;
RT   "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT   precursor of Mus domesticus.";
RL   Nucleic Acids Res. 17:5396-5396(1989).
RN   [9]
RP   SEQUENCE OF 656-737 FROM N.A.
RC   STRAIN=129/Sv;
RA   Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA   Loring J.F., Goate A.M.;
RT   "Introduction of six mutations into the mouse genome using 'Hit and
RT   Run' gene-targeting: introduction of familial Alzheimer's disease
RT   mutations into the mouse amyloid precursor protein gene and
RT   humanization of the A-beta fragment.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX   MEDLINE=93287808; PubMed=8510506;
RA   Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT   "Regional distribution of the alternatively spliced isoforms of beta
RT   APP RNA transcript in the brain of normal, heterozygous and
RT   homozygous weaver mutant mice as revealed by in situ hybridization
RT   histochemistry.";
RL   Brain Res. Mol. Brain Res. 17:340-346(1993).

RN   [11]
RP   INTERACTION WITH KNS2.
RX   MEDLINE=21010507; PubMed=11144355;
RA   Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT   "Axonal transport of amyloid precursor protein is mediated by direct
RT   binding to the kinesin light chain subunit of kinesin-I.";
RL   Neuron 28:449-459(2000).
RN   [12]
RP   C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP   THR-743; TYR-757; ASN-759 AND TYR-762.
RX   MEDLINE=21408156; PubMed=11517249;
RA   Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA   Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA   Kyriakis J.M., Nishimoto I.;
RT   "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT   scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL   J. Neurosci. 21:6597-6607(2001).
RN   [13]
RP   INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX   MEDLINE=22028091; PubMed=11912189;
RA   Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT   "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT   with scaffold proteins of the JNK signaling cascade.";
RL   J. Biol. Chem. 277:20070-20078(2002).
RN   [14]
RP   INTERACTION OF CTF PEPTIDES WITH NUMB.
RX   MEDLINE=22008109; PubMed=12011466;
RA   Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA   Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT   "The gamma-secretase-generated intracellular domain of beta-amyloid
RT   precursor protein binds Numb and inhibits Notch signaling.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN   [15]
RP   GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX   MEDLINE=21437805; PubMed=11553691;
RA   Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT   "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT   gamma-secretase is rapidly degraded but distributes partially in a
RT   nuclear fraction of neurones in culture.";
RL   J. Neurochem. 78:1168-1178(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC   physiological functions on the surface of neurons relevant to
CC   neurite growth, neuronal adhesion and axonogenesis. Involved in
CC   cell mobility and transcription regulation through protein-protein
CC   interactions. Can promote transcription activation through binding
CC   to APBB1/Tip60 and inhibit Notch signaling through interaction
CC   with Numb. Couples to apoptosis-inducing pathways such as those
CC   mediated by G(O) and JIP. Inhibits G(0) alpha ATPase activity (By
CC   similarity). Acts as a kinesin I membrane receptor, mediating the
CC   axonal transport of beta-secretase and presenilin 1. May be
CC   involved in copper homeostasis/oxidative stress through copper ion
CC   reduction. Can regulate neurite outgrowth through binding to
CC   components of the extracellular matrix such as heparin and
CC   collagen I and IV (By similarity). The splice isoforms that
CC   contain the BPTI domain possess protease inhibitor activity (By
CC   similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

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CC          with metal-reducing activity. Bind transient metals such as
CC          copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC          only weakly transient metals and have little reducing activity due
CC          to substitutions of transient metal chelating residues. Beta-APP42
CC          may activate mononuclear phagocytes in the brain and elicit
CC          inflammatory responses. Promotes both tau aggregation and TPK II-
CC          mediated phosphorylation (By similarity).
CC    -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC          peptides, including C31, are potent enhancers of neuronal
CC          apoptosis.
CC    -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC          cytoplasmic proteins, including APBB family members, the APBA
CC          family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC          its serine phosphorylation. Also interacts with GPCR-like protein
CC          BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
CC          BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC          MT-binding domains (By similarity). Associates with microtubules
CC          in the presence of ATP and in a kinesin-dependent manner (By
CC          similarity). Interacts, through a C-terminal domain, with GNAO1
CC          (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC          neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC          similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC          protein that rapidly becomes internalized via clathrin-coated
CC          pits. During maturation, the immature APP (N-glycosylated in the
CC          endoplasmic reticulum) moves to the Golgi complex where complete
```

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  Query Match              100.0%;  Score 40;  DB 1;  Length 770;
  Best Local Similarity    100.0%;  Pred. No. 0.38;
    Matches      8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps      0;

Qy          1 KLVFFAED 8
              ||||||||
Db        687 KLVFFAED 694
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RESULT 11
A4_PIG
ID   A4_PIG          STANDARD;       PRT;    770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
```

RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC   physiological functions on the surface of neurons relevant to
CC   neurite growth, neuronal adhesion and axonogenesis. Involved in
CC   cell mobility and transcription regulation through protein-protein
CC   interactions (By similarity). Can promote transcription activation
CC   through binding to APBB1/Tip60 and inhibit Notch signaling through
CC   interaction with Numb (By similarity). Couples to apoptosis-
CC   inducing pathways such as those mediated by G(O) and JIP (By
CC   similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC   Acts as a kinesin I membrane receptor, mediating the axonal
CC   transport of beta-secretase and presenilin 1 (By similarity). May
CC   be involved in copper homeostasis/oxidative stress through copper
CC   ion reduction (By similarity). In vitro, copper-metallated APP
CC   induces neuronal death directly or is potentiated through Cu(II)-
CC   mediated low-density lipoprotein oxidation (By similarity). Can
CC   regulate neurite outgrowth through binding to components of the
CC   extracellular matrix such as heparin and collagen I and IV (By
CC   similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC   with metal-reducing activity. Bind transient metals such as
CC   copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC   peptides, including C31, are potent enhancers of neuronal
CC   apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC   cytoplasmic proteins, including APBB family members, the APBA
CC   family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC   to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC   interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC   (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC   In vitro, it binds MAPT via the MT-binding domains (By
CC   similarity). Associates with microtubules in the presence of ATP
CC   and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC   protein that rapidly becomes internalized via clathrin-coated
CC   pits. During maturation, the immature APP (N-glycosylated in the
CC   endoplasmic reticulum) moves to the Golgi complex where complete
CC   maturation occurs (O-glycosylated and sulfated). After alpha-
CC   secretase cleavage, soluble APP is released into the extracellular

CC   space and the C-terminal is internalized to endosomes and
CC   lysosomes. Some APP accumulates in secretory transport vesicles
CC   leaving the late Golgi compartment and returns to the cell
CC   surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC   and nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC   sorting of membrane proteins to the basolateral surface of
CC   epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC   phosphorylated proteins is required for the specific binding of
CC   the PID domain. However additional amino acids either N- or C-
CC   terminal to the NPXY motif are often required for complete
CC   interaction. The PID domain-containing proteins which bind APP
CC   require the YENPTY motif for full interaction. These interactions
CC   are independent of phosphorylation on the terminal tyrosine
CC   residue. The NPXY site is also involved in clathrin-mediated
CC   endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC   Cleavage by alpha-secretase or alternatively by beta-secretase
CC   leads to generation and extracellular release of soluble APP
CC   peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC   retention of corresponding membrane-anchored C-terminal fragments,
CC   C83 and C99. Subsequent processing of C83 by gamma-secretase
CC   yields P3 peptides. This is the major secretory pathway and is
CC   nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC   gamma-secretase processing of C99 releases the amyloid beta
CC   proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC   major components of amyloid plaques, and the cytotoxic C-terminal
CC   fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC   similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC   (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC   results in the production of the neurotoxic C31 peptide and the
CC   increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC   serine residues is neuron-specific. Phosphorylation can affect APP
CC   processing, neuronal differentiation and interaction with other
CC   proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC   corresponding oxidation of Cys-144 and Cys-158, and the formation
CC   of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC   zinc, can induce histidine-bridging between beta-amyloid molecules
CC   resulting in beta-amyloid-metal aggregates (By similarity).
CC   Extracellular zinc-binding increases binding of heparin to APP and
CC   inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---

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CC      ----------------------------------------------------------------------
DR      EMBL; AB032550; BAA84580.1; -.
DR      EMBL; Z84022; CAB06313.1; -.
DR      EMBL; X56127; CAA39592.1; -.
DR      HSSP; P05067; 1AAP.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW      Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW      Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW      Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW      Amyloid.
FT      SIGNAL          1       17      BY SIMILARITY.
FT      CHAIN          18      770      AMYLOID BETA A4 PROTEIN.
FT      CHAIN          18      687      SOLUBLE APP-ALPHA (POTENTIAL).
FT      CHAIN          18      671      SOLUBLE APP-BETA (POTENTIAL).
FT      CHAIN         672      770      C99 (BY SIMILARITY).
FT      CHAIN         672      713      BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT      CHAIN         672      711      BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT      CHAIN         688      770      C83 (BY SIMILARITY).
FT      CHAIN         688      713      P3(42) (BY SIMILARITY).
FT      CHAIN         688      711      P3(40) (BY SIMILARITY).
FT      CHAIN         712      770      GAMMA-CTF(59).
FT      CHAIN         714      770      GAMMA-CTF(57).
FT      CHAIN         721      770      GAMMA-CTF(50) (BY SIMILARITY).
FT      CHAIN         740      770      C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT      DOMAIN         18      699      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      700      723      POTENTIAL.
FT      DOMAIN        724      770      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN         96      110      HEPARIN-BINDING (BY SIMILARITY).
FT      DOMAIN        135      155      COPPER-BINDING (BY SIMILARITY).
FT      DOMAIN        181      188      ZINC-BINDING (BY SIMILARITY).
FT      DOMAIN        291      341      BPTI/KUNITZ INHIBITOR.
FT      DOMAIN        391      423      HEPARIN-BINDING (BY SIMILARITY).
FT      DOMAIN        491      522      HEPARIN-BINDING (BY SIMILARITY).
FT      DOMAIN        523      540      COLLAGEN-BINDING (BY SIMILARITY).
FT      DOMAIN        732      751      INTERACTION WITH G(O)-ALPHA (BY
FT                                      SIMILARITY).
FT      DOMAIN        230      260      ASP/GLU-RICH (ACIDIC).
FT      DOMAIN        274      280      POLY-THR.
FT      SITE          144      144      REQUIRED FOR COPPER(II) REDUCTION
FT                                      (BY SIMILARITY).
FT      ACT_SITE      301      302      REACTIVE BOND (BY SIMILARITY).
FT      SITE          671      672      CLEAVAGE (BY BETA-SECRETASE)
FT                                      (BY SIMILARITY).
FT      SITE          672      673      CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT      SITE          687      688      CLEAVAGE (BY ALPHA-SECRETASE)
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FT                               (BY SIMILARITY).
FT     SITE      704    704      IMPLICATED IN FREE RADICAL PROPAGATION
FT                               (BY SIMILARITY).
FT     SITE      706    706      INVOLVED IN OXIDATIVE REACTIONS
FT                               (BY SIMILARITY).
FT     SITE      711    712      CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                               (BY SIMILARITY).
FT     SITE      713    714      CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                               (BY SIMILARITY).
FT     SITE      720    721      CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

   Query Match              100.0%;  Score 40;  DB 1;  Length 770;
   Best Local Similarity    100.0%;  Pred. No. 0.38;
   Matches     8;  Conservative     0;  Mismatches     0;  Indels     0;  Gaps     0;


Qy         1 KLVFFAED 8
             | | | | | | | |
Db       687 KLVFFAED 694



RESULT 12
A4_RAT
ID   A4_RAT            STANDARD;      PRT;    770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE   amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE   C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE   fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE   Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN   APP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88312583; PubMed=2900758;
RA   Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA   Seeburg P.H.;
RT   "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT   in rat brain suggests a role in cell contact.";
RL   EMBO J. 7:1365-1370(1988).
RN   [2]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89183625; PubMed=2648331;
RA   Kang J., Mueller-Hill B.;
RT   "The sequence of the two extra exons in rat preA4.";
RL   Nucleic Acids Res. 17:2130-2130(1989).
RN   [3]
RP   SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
```

RX   MEDLINE=21443797; PubMed=11483588;
RA   Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT   "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT   family resembling gamma-secretase-like cleavage of Notch.";
RL   J. Biol. Chem. 276:35235-35238(2001).
RN   [4]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=96187032; PubMed=8624099;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "APP gene family. Alternative splicing generates functionally related
RT   isoforms.";
RL   Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN   [5]
RP   TISSUE SPECIFICITY OF APPICAN.
RX   MEDLINE=95263526; PubMed=7744833;
RA   Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA   Mytilineou C., Margolis R.U., Robakis N.K.;
RT   "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT   brain and is produced by astrocytes but not by neurons in primary
RT   neural cultures.";
RL   J. Biol. Chem. 270:11839-11844(1995).
RN   [6]
RP   TISSUE SPECIFICITY OF ISOFORMS.
RX   MEDLINE=97150061; PubMed=8996834;
RA   Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT   "Expression of the APP gene family in brain cells, brain development
RT   and aging.";
RL   Gerontology 43:119-131(1997).
RN   [7]
RP   INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP   TYR-762.
RX   MEDLINE=99127916; PubMed=9930726;
RA   Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA   Suzuki T., Nairn A.C., Greengard P.;
RT   "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT   Alzheimer's amyloid precursor protein.";
RL   J. Neurochem. 72:549-556(1999).
RN   [8]
RP   INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
RX   MEDLINE=99162676; PubMed=10024358;
RA   Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA   Valenza C., Prochiantz A., Allinquant B.;
RT   "The amyloid precursor protein interacts with Go heterotrimeric
RT   protein within a cell compartment specialized in signal
RT   transduction.";
RL   J. Neurosci. 19:1717-1727(1999).
RN   [9]
RP   CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX   MEDLINE=95256193; PubMed=7737970;
RA   Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT   "The chondroitin sulfate attachment site of appican is formed by
RT   splicing out exon 15 of the amyloid precursor gene.";
RL   J. Biol. Chem. 270:10388-10391(1995).
RN   [10]
RP   BETA-AMYLOID METAL-BINDING.
RX   MEDLINE=99316162; PubMed=10386999;
RA   Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,

RA   Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA   Bush A.I.;
RT   "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT   peroxide through metal ion reduction.";
RL   Biochemistry 38:7609-7616(1999).
RN   [11]
RP   BETA-AMYLOID ZINC BINDING.
RX   MEDLINE=99343552; PubMed=10413512;
RA   Liu S.T., Howlett G., Barrow C.J.;
RT   "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT   of the A beta peptide of Alzheimer's disease.";
RL   Biochemistry 38:9373-9378(1999).
RN   [12]
RP   IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP   GLY-704.
RX   MEDLINE=21956095; PubMed=11959460;
RA   Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT   "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT   peptide 1-42-associated oxidative stress and neurotoxicity.";
RL   Biochim. Biophys. Acta 1586:190-198(2001).
RN   [13]
RP   PHOSPHORYLATION.
RX   MEDLINE=97239592; PubMed=9085254;
RA   Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA   Greengard P., Suzuki T.;
RT   "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT   phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT   cultured cells.";
RL   Mol. Med. 3:111-123(1997).
RN   [14]
RP   PHOSPHORYLATION ON SER-730.
RX   MEDLINE=99262094; PubMed=10329382;
RA   Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA   Greengard P., Nairn A.C., Suzuki T.;
RT   "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT   precursor protein at Ser655 by a novel protein kinase.";
RL   Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN   [15]
RP   PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP   THR-743.
RX   MEDLINE=99274744; PubMed=10341243;
RA   Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA   Kirino Y., Greengard P., Suzuki T.;
RT   "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT   during neuronal differentiation.";
RL   J. Neurosci. 19:4421-4427(1999).
RN   [16]
RP   PHOSPHORYLATION ON THR-743.
RX   MEDLINE=20396183; PubMed=10936190;
RA   Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA   Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT   "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT   protein by cyclin-dependent kinase 5.";
RL   J. Neurochem. 75:1085-1091(2000).
RN   [17]
RP   CARBOHYDRATE STRUCTURE OF APPICAN.
RX   MEDLINE=21463085; PubMed=11479316;

RA   Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA   Sugahara K., Robakis N.K.;
RT   "Appican, the proteoglycan form of the amyloid precursor protein,
RT   contains chondroitin sulfate E in the repeating disaccharide region
RT   and 4-O-sulfated galactose in the linkage region.";
RL   J. Biol. Chem. 276:37155-37160(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC   physiological functions on the surface of neurons relevant to
CC   neurite growth, neuronal adhesion and axonogenesis. Involved in
CC   cell mobility and transcription regulation through protein-protein
CC   interactions (By similarity). Can promote transcription activation
CC   through binding to APBB1/Tip60 and inhibit Notch signaling through
CC   interaction with Numb (By similarity). Couples to apoptosis-
CC   inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC   G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC   mediating the axonal transport of beta-secretase and presenilin 1
CC   (By similarity). May be involved in copper homeostasis/oxidative
CC   stress through copper ion reduction. Can regulate neurite
CC   outgrowth through binding to components of the extracellular
CC   matrix such as heparin and collagen I and IV (By similarity). The
CC   splice isoforms that contain the BPTI domain possess protease
CC   inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC   with metal-reducing activity. Bind transient metals such as
CC   copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC   only weakly transient metals and have little reducing activity due
CC   to substitutions of transient metal chelating residues. Beta-APP42
CC   may activate mononuclear phagocytes in the brain and elicit
CC   inflammatory responses. Promotes both tau aggregation and TPK II-
CC   mediated phosphorylation (By similarity).
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC   extracellular matrix and may regulate neurite outgrowth in the
CC   brain.
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC   peptides, including C31, are potent enhancers of neuronal
CC   apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC   cytoplasmic proteins, including APBB family members, the APBA
CC   family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC   to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC   interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC   (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC   In vitro, it binds MAPT via the MT-binding domains (By
CC   similarity). Associates with microtubules in the presence of ATP
CC   and in a kinesin-dependent manner (By similarity). Interacts,
CC   through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC   CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC   associates with HADH2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC   protein that rapidly becomes internalized via clathrin-coated
CC   pits. During maturation, the immature APP (N-glycosylated in the

Query Match   100.0%; Score 40; DB 1; Length 770;
Best Local Similarity   100.0%; Pred. No. 0.38;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8

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         |||||||
Db       687 KLVFFAED 694


RESULT 13
A4_TETFL
ID   A4_TETFL        STANDARD;      PRT;    780 AA.
AC   O73683;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Tetraodon fluviatilis (Puffer fish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
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DR    PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR    PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW    Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW    Serine protease inhibitor.
FT    SIGNAL         1      18        POTENTIAL.
FT    CHAIN         19     780        ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                    HOMOLOG.
FT    CHAIN        682     724        BETA-AMYLOID PROTEIN (POTENTIAL).
FT    DOMAIN        19     711        EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM     712     732        POTENTIAL.
FT    DOMAIN       733     780        CYTOPLASMIC (POTENTIAL).
FT    DOMAIN       323     382        BPTI/KUNITZ INHIBITOR.
FT    SITE         769     772        CLATHRIN-BINDING (BY SIMILARITY).
FT    DISULFID     327     378        BY SIMILARITY.
FT    DISULFID     336     361        BY SIMILARITY.
FT    CARBOHYD     560     560        N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ    SEQUENCE     780 AA;    88238 MW;   60071BE94520191D CRC64;

    Query Match              100.0%;   Score 40;   DB 1;   Length 780;
    Best Local Similarity    100.0%;   Pred. No. 0.38;
    Matches    8;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy         1 KLVFFAED 8
             ||||||||
Db       697 KLVFFAED 704


RESULT 14
A4_FUGRU
ID    A4_FUGRU        STANDARD;      PRT;    737 AA.
AC    O93279;
DT    10-OCT-2003 (Rel. 42, Created)
DT    10-OCT-2003 (Rel. 42, Last sequence update)
DT    10-OCT-2003 (Rel. 42, Last annotation update)
DE    Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE    Beta-amyloid protein (Beta-APP) (A-beta)].
GN    APP.
OS    Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC    Tetraodontoidea; Tetraodontidae; Takifugu.
OX    NCBI_TaxID=31033;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=98252138; PubMed=9599080;
RA    Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT    "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL    Gene 210:17-24(1998).
CC    -!- FUNCTION: Functional neuronal receptor which couples to
CC        intracellular signaling pathway through the GTP-binding protein
CC        G(O) (By similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    -!- SIMILARITY: Belongs to the APP family.
CC    -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC    -------------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR   EMBL; AF090120; AAD13392.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL   1   18   POTENTIAL.
FT   CHAIN   19   737   ALZHEIMER'S DISEASE AMYLOID A4
FT   PROTEIN HOMOLOG.
FT   CHAIN   639   681   BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN   19   668   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   669   689   POTENTIAL.
FT   DOMAIN   690   737   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   286   344   BPTI/KUNITZ INHIBITOR.
FT   SITE   726   729   CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE   300   301   REACTIVE BOND.
FT   DISULFID   290   340   BY SIMILARITY.
FT   DISULFID   299   323   BY SIMILARITY.
FT   DISULFID   315   336   BY SIMILARITY.
FT   CARBOHYD   522   522   N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   737 AA;   82856 MW;   6FAD01E2E3B2B7E2 CRC64;

     Query Match   92.5%; Score 37; DB 1;   Length 737;
     Best Local Similarity   87.5%; Pred. No. 1.7;
     Matches   7; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||:|
Db   654 KLVFFADD 661

RESULT 15
Y189_RICPR
ID   Y189_RICPR   STANDARD;   PRT;   321 AA.
AC   Q9ZDX5;
DT   30-MAY-2000 (Rel. 39, Created)

    Query Match   85.0%; Score 34; DB 1; Length 321;
    Best Local Similarity   75.0%; Pred. No. 3.7;
     Matches   6; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
            ||:||| |
Db   178 KLIFFAHD 185

Search completed: March 4, 2004, 15:36:26
Job time : 1.25532 secs